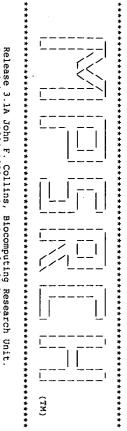
US38183-1-38183

MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGELMTLAT WUGUNLEDPASRDLVYSYVNTNMGLKFROLLWFHISCLTFGRETVIEYLVSFGVWIRTPPAYRPPNAPIL STLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRESQCEIIRDGFLLLQMDFGFFPEHLLVDFLQ SLSMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGELMT LATWYGVNLEDPASRDLVYSYVNTNMGLKFROLLDTASALYFGRETVIEYLVSFGVWIRTPPAYRPPNA PILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRESQC1

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 16 12:43:38 1999: MasPar time 17.14 Seconds 491.237 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

Sequence: >US38183-1-38183 (1736) from us38183-1-38183.pep 2977 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 396

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 33.376; Variance 170.298; scale 0.196

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result
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                                                                                                                                                                     PT DNA encoding proteins which can be incorporated with wild type mincleocapsid subunit(s) into a viral nucleocapsid - useful for inhibition of viral replication, especially hepatitis B virus PS Claim 15; Page 35; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25) protein that is encoded by the full-length HBV precore gene. Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsids along thin the p21 core protein (see W50251), which is the usual nucleocapsid component, and thereby render the nucleocapsids deficient in encapsidating HBV pregenomic RNA. Thus, overexpression of the precore proteins, or certain variants of them, cappression of the precore proteins, or certain variants of them, cappression of the precore proteins of HBV replication. Suitable cappression of the precore proteins of HBV pregenomic RNA. Thus, overexpression of the precore proteins of HBV pregenomic RNA. Thus, overexpression of the precore proteins of HBV pregenomic RNA. Thus, overexpression of the precore proteins of HBV pregenomic RNA. Thus, overexpression of them, suitable of the precore proteins of HBV pregenomic RNA. Thus, overexpression of them, suitable of the precore proteins of the precore by them, suitable of the precore proteins of the precore by them, suitable of the precore proteins of the precore proteins of the precore by them, suitable of the precore proteins of the
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Sequence 194 AA;
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03-SEP-1996; US-025370.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, Wands JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatocyte; liver; p25 protein.
Hepatitis B virus.
W09809649-A1.
12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus precore p25 polypeptide.
Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
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SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI
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99.5%;
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Pred. No. 1.53e-101;
1; Mismatches 0;
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ID R27473 standard; Proc...

AC R27473;

AC R27473;

DT 24-FEB-1993 (first entry)

DE S12/core protein.

KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;

KW vaccinia virus; I3L; promoter; NYVAC; recombinant; HBV L;

KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;

KW large pre-S antigen; lpsAg; fusion protein; vaccinia virus; virulence factor;

S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;

""" S1; S2; copenhagen vaccine strain; vaccinia virus; virulence factor;
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                                                                                             PT Vaccinating against viral infections such as rables, hepatitis B, PT HIV, HSV, EBV, CMV, numps etc.

PS Disclosure; Fig 13; 456pp; English.

CC The sequence given is encoded by an expression cassette which comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/CC core) which is precisely linked to the IJL promoter derived from CC core, which is precisely linked to the HBL promoter derived from CC vaccinia virus. This DNA sequence was linked to the S1 and S2 countries and this fragment was used in the construction of a NYVAC sequences and this fragment was used in the construction of a NYVAC in the construction. These were HBV m protein (small pre-S antigen, SpsAg) and HBV L (large pre-S antigen, 198Ag). Each of these gene containing essential genes. NYVAC is separated by from each other by large regions of vaccinia DNA containing essential genes. NYVAC is deletion of six non-essential regions of the genome encoding known or potential virulence factors. The deletion to impress the spacing of the three inserted sequences ensured that any recombination that did occur would lead to disruption of the construction of the construction and would cause unviable vaccinia virus. See also
   Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09215672-A.
17-SEP-1992.
09-MAR-1992; U01906.
07-MAR-1991; US-666056.
11-JUN-1991; US-713967.
06-MAR-1992; US-847951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (VIRO-) VIROGENETICS CORP.
COX WI, De Taisne C, Francis J, Gettig RR, Johnson GI
Limbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus
Riviere M, Tartaglia J, Taylor J;
WPI; 92-331718/40.
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                                                                                  vaccinia genome and would Q35501-864.
                                                                    Sequence
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larity 99.5%;
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164..346
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20-JUN-1995; U10602.

20-JUN-1995; US-017814.

(GEHO ) GEN HOSPITAL CORP.

Melegari M. Scaglioni PP,

WPI: 97-087176/08.
                                                                                                                                                                                                                                   Disclosure; Page 46-48: 83pp; English.

Plasmid phBv DN AA carries an insert (T49598) coding for a prot (W09048) comprising a hepatitis B virus (HBV) core protein (see also W09044) fused in-frame at amino acid 179 with the HBV suri protein (see also W09045) at amino acid 8. Plasmid phBv DN BB (T49599) expresses the HBV core fused at amino acid 175 to the surface protein at amino acid 112 (W09049). phBv DN AA was at least as potent an inhibitor of HBV replication as construct pHBV DN (T49597); phBV DN BB was less inhibitory than pHBV DN. Vectors expressing hepadnavirus dominant negative core mutants be utilised in the gene therapy of viral infections.

Sequence 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid phBV DN AA encoded HBV dominant negative polypeptide. Hepadnavirus; woodchuck hepatitis virus; hepatitis delta virus; HBV; ground squirrel hepatitis B virus; duck hepatitis B virus; core protein; replication; antiviral; gene therapy; pHBV DN AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          New method for inhibiting the replication of hepadnaviruses - comprises introducing a mutant polypeptide with a mutated core protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T49598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09048 standard;
W09048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-1997
                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343
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                                                                                                                                                                              Local Similarity
mes 185; Consen
                                                                                                                                                                                                        Match
                                                                                                                                 mdidpykefgatvellsflpsdffpsvrdlldtasalyrealespehcsphhtalrqail 60
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 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRE
                   sfgvwirtppayrppnapilstlpettvvrrrgrsprrrtpsprrrrsqsprrrrsqsrl
                                                            CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
                                                                           MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346
                                                                                                                                                                           46.2%;
larity 90.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= HBV_core
/note= "positions 1-179
1-179 of HBV core protes
180..397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "positions 180-397 correspond
9-226 of HBV surface protein"
                                                                                                                                                                           Score
Pred.
8; M
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                                                                                                                                                                           re 1375; DB 20;
d. No. 1.53e-101;
Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-179 correspond protein"
                                                                                                                                                                              10;
                                                                                                                                                                                                        Length
                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                 for a protein
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surface
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RESULT
ID WI
AC WI
AC V
DT 28
DE H6
KW V
KW h6
FT K6
FT R6
FT R6
PD 11
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PA (SCRI-) Scripps Clinic Res.

PT Thornton GB, Moriarty AM, Millich DR, McLachlan A.;

PPT Mbriton GB, Moriarty AM, Millich DR, McLachlan A.;

PPT New conjugates and fusion proteins of immunogenic polypeptide -

PPT and hepatitis B core antigen, useful in vaccines.

PPT and hepatitis B core antigen, useful in vaccines.

PS Disclosure; p; English.

CC This sequence contains the T cell stimulating epitopes, amino acid

CT This sequence contains the T cell stimulating epitopes, amino acid

CT This sequence contain determinants that suppress T cell activation.

PS Disclosure; p; English.

CC This sequence sesentially consisting of 15 to 55 amino acids

CC TO-140 do not contain determinants that suppress T cell activation.

CC Polypeptides essentially consisting of 15 to 55 amino acids

CC corresponding to the above mentioned HBV regions are T cell

CC stimulating. Coupling a polypeptide immunogen to such sequences,

CC e.g. by using a bifunctional reagent which forms a disulphide link,

CC improves its immunogenicity. These are useful in vaccines and can be us

CC therapeutically to improve T cell response to HBCAg in infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subjects.
See also
Sequence
  WO9809649-A1.
12-MAR-1998.
                                                                                                                                            Viral replication; inhibitor; HBV; i hepatocyte; liver; p21; core protei Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-1988.
07-DEC-1987; 310725.
07-OCT-1987; US-106538.
07-OCT-1987; US-939617.
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EP-271302-A.
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                                                                                                                                                                                                                                                             W50251;
28-SEP-1998
                                                                                                                                                                                                                                                                                                                         W50251 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P80959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ESQC
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                                                                                                                                                                                                                                                                                                                                                    σ
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183; Conser
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184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       183
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llarity 99.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                      Protein; 183
                                                                                                                 location/Qualifiers
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                                                                                                                                                                          core protein
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Pred. No. 1.53e-100;
                                                                                                                                                                                                    nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HBV subtype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT DNA encoding proteins which can be incorporated with wild type proteins could be protein a viral nucleocapsid - useful for prinhibition of viral replication, especially hepatitis B virus PS Disclosure; Page 41-42; 60pp; English.

CC This is the 21 kDa (p21) protein of hepatitis B virus (HBV) that CC assembled into a 180 kSa subunit nucleocapsid structure that CC promotes viral replication. Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV CC precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsids along with the p21 core protein and thereby render the nucleocapsids along with the p21 core protein core protein variants of them, leads to transdominant inhibition of HBV CC pregenomic RNA. Thus, over-expression of the precore proteins or CC certain variants of them, leads to transdominant inhibition of HBV CC wettors and host cells, and can be provided expension can be produced by recombinant methods using claimed expression collect acid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV creation.
      D 12-MAR-1998.

F 03-SEP-1997; U15500.

R 03-SEP-1996; U5-025370.

R (GEHO ) GEN HOSPITAL CORP.

I Melegari M, Scaglioni PP, Wands JR;

I Molecoapsid Subunit(s) into a viral nucleocapsid - useful for nucleocapsid subunit(s) into a viral nucleocapsid - useful for inhibition of viral replication, especially hepatitis B virus S Claim 9; Page 34-35; 60pp; English.

S Claim 9; Page 34-35; 60pp; English.

C This polypeptide comprises the hepatitis B virus (HBV) 22 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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03-SEP-1996; US-025370.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, W
WPI; 98-193325/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis B virus precore p22 polypeptide. Viral replication; inhibitor; HBV; nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W50241 standard; Protein; 193
                                                                                                                                                                                                                                                                                                                                                                      WO9809649-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatocyte;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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nes 181; Consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   liver; p22 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.6%;
llarity 98.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 82..98
                                                                                                                                                                                                                                                                                                                                                                                                     "immunodominant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1358; DB 32;
Pred. No. 3.99e-100;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                          hepatitis B virus (HBV) 22 kDa (p22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                  useful for is B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein that is produced by elimination of the 19-amino acid leader peptide from the 25 kDa full-length HBV precore protein (see W50250). Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsids along with the p21 core protein (see W50251), which is the usual nucleocapsid to component, and thereby render the nucleocapsids deficient in encapsidating HBV pregenomic RNA. Thus, over-expression of the precore proteins, or certain variants of them, cleads to transdominant inhibition of HBV replication. Suitable inhibitory proteins include p25 (see W50250), p22, Met-p22 (see w50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het (see W50238). Heterologous peptides (see W50237) and Met-p18-Het (see W50238). Heterologous peptides (see W50237) and peptides (see W50238). Heterologous peptides (see W50237) and met-p18 proteins can be produced by recombinant methods using claimed expression vectors and host cells. They can be provided exogenously to the target cells for use in inhibiting HBV replication.

Can Alternatively, a nucleic acid construct that directs overexpression of any inhibitory protein in target cells is used for the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local (
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Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta ground squirrel hepatitis B virus; duck hepatitis B virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09044 standard; Protein; 183 AA. W09044; 11-APR-1997 (first entry)
                                                                                 misc_difference
                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        core protein; replication; antiviral; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lcwgelmtlatwvgvnledpasrdlvvsyvdtnmglkfrqllwfmiscltfgretvieyl 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%;
1 Similarity 98.4%;
181; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of HBV
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                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "C-terminus of core protein is acid position between 71-180 in mutant polypeptides of the invention (Claim 22 81.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection.
                                                                                    acid position between 174 and 180 in polypeptides of the invention (Claim 178
                                                                                                                                                                                                                                                                                                             acid position between polypeptides of the in 171..180
                                                                                                                                                                                                  /note= "C-terminus of core protein is at any acid position between 171 and 180 in mutant polypeptides of the invention (Claim 6)" 174..180
  position 178 invention (C)
                                                          /note= "C-terminus of
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
  (Claim
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Pred. No. 3.
        in mutant
laim 7)"
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                                                                                                                                                                                                                                                                                                                                             invention
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                                                            core
                             core protein is at amino polypeptides of the
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3.29e-100;
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26)"
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                                                                        27-JUN-1990.

1-JAN-1999; 123526.

2-DEC-1978; GB-049907.

27-DEC-1978; GB-050039.

01-NOV-1979; GB-037910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 55-56; 83pp; English.

Claim 5; Page 55-56; 83pp; English.

Alteration of the C-terminus of the core protein (W09044) of Alteration of the C-terminus of the core protein of the wild-type virus polypeptide capable of reducing replication of the wild-type virus by a dominant negative mechanism. The inhibitory effect is species-specific and is achieved by deletion of a few C-terminal amino acids from the core protein, and/or by joining the core protein to a hepadnavirus surface protein (see also W09045), protein to a hepadnavirus surface fusion. Such mutant polypeptides (see
                                  (BIOJ) Biogen Inc.
Murray K, Schaller HE;
WPI; 90-195067/26.
 Recombinant DNA encoding Hepatitis B virus polypeptide antigens used in detection of infection and in vaccine prodn.
                          WPI; 90-195067
N-PSDB; Q04799
                                                                                                                                                                 Hepatitis B
Hepatitis B
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New method for inhibiting the replication of hepadnaviruses comprises introducing a mutant polypeptide with a mutated or protein or corresponding nucleic acid, for treating, e.g. h
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                                                                                                                                         EP-374869-A.
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09-JAN-1997.
20-JUN-1996; U10602.
20-JUN-1995; US-017814.
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181; Conser
                                                                                                                                                                                                                  standard;
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                                                                                                                                                                 virus; va
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larity 98.98;
Conservative
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position 178 in mutant polypeptides
invention (Claim 7)"
172..183
/note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "amino acid residues 172-183,
are deleted from the core protein in
polypeptides of the invention"
                                                                                                                                                                                                                 protein;
                                                                                                                                                                 vaccine; HBV;
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Pred.
0; N
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. No. 1.04e-99;
Mismatches 2;
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e.g. hepatitis
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Best Local S
Matches 17
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Best I
                                                                                                                  Matches
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EP-13828-A.
06-AUG-1980.
21-DEC-1979; 303017.
22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
(BIOJ) BIOGEN NV.
MUTTAY K, Schaller HE;
WPI: 80-57268C/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure: Polypeptide 1
HBV and may 1
Cultured in 1
                                                                                                                                                                      Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Example; Figs 3-4; 43pp; English. Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contg, pellet which was labelled with 3H or 3P as described by Raplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of Hepatitis
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                    MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 45.3%;
l Similarity 96.7%;
177; Conservative
                                                                                                                 l Similarity
177; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                        8 8 ct
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (first entry)
f core antigen.
B virus; antigen;
B virus.
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f the sequence are also claimed as being antigenicall
                                                                                                               45.3%;
llarity 96.7%;
Conservative
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                                                                                                              Score 1349; DB 5;
Pred. No. 2.24e-99;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody;
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Pred. No. 2.24e-99;
5; Mismatches
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RESULPT AND SELECTION OF SELECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PT Recombinant DNA coding for polypeptide - have specificity of PT hepatitis B viral antigens in detection or antibody stimulation PS Claim 13; Page 40; 43pp; English.

CC Human serum from a single HBSAq positive, HBeAq positive donor CC (serotype adym) was used to prep. a DNA-contg. pellet which was CC labelled with 3H or 32p as described by P. M. Kaplan et al (1973).

CC The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).

CC It was then cloned in plasmid pBR322 which was used to transform E.

CC coli. Micro-organisms prepd. by the processes are deposited at the CNCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-PSt I dG:

CC HBV-Kpn I dC: Tetr AmpS HBV+.
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Best Local Similarity
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R40806;
R40806;
16-FEB-1994
                                                                                                                                                                       Hepatitis
Hepatitis
Synthetic.
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22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
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Sequence of core antigen.
Hepatitis B virus; antigen;
Hepatitis B virus.
                             J05192170-A
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Murray K, Schaller HE;
WPI; 80-57268C/33.
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P00004 standard; Protein; 184
                                                                             protein
                                                                                                                            region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
                                                                                                                                                                                                                                                                                                 standard; Protein; 196
                                                                                                                                                                                             B core / PV-1 fusion B; core; HBC; PV-1;
                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                           184
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larity 96.2%;
Conservative
                                                                                                                                                                                                                      (first entry)
core / PV-1 fusion.
                                                                          /label= PV-1
14..196
                                                                                                                                                Location/Qualifiers
                                                      · HBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1338;
Pred. No. 1.
5; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody; diagnosis;
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                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                  IL-1
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                                                                                                                                                                                                  beta; interleukin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
L.85e-98;
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24 igmdidpykefgasvellsflpsdffpsirdlldtasalyrealespehcsphhtalrqa 83

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Best Local Similarity 94.6%;
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 44.9%;
Best Local Similarity 95.1%;
Matches 175; Conservative
                                                                                                                                                          (NISW ) NISSHIN OIL MILLS I. WPI; 93-277479/35.
N-PSDB; Q47738.
                                                                                                                                                                                                                                                                                                                                                       R40808 standard; Protein; 208 A
R40808;
16-FEB-1994 (first entry)
Hepatitis B core / PV-1 / IL-1
Hepatitis B; core; HBC; PV-1; I
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS L
WPI; 93-277479/35.
N-PSDB; Q47736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus and exetic genes
Disclosure; Fig 7; 12pp; Japanese.
The hepatitis B core gene is recombined with pv-1 DNA
and IL-1 beta to form a plasmid (047738) which is then used to
a vaccine. NB: Sequence is difficult to read in the original
specification.
                                                                                                                                                                                                             J05192170-A.
03-AUG-1993.
24-SEP-1991;
24-SEP-1991;
                                                                           Recombinant plasmid for high immunogenity virus - contains recombined haemagglutinin gene, hepatitis B core gene of vacvirus and exotic genes
Disclosure; Fig 9; 12pp; Japanese.
The hepatitis B core gene is recombined with pv-1 DNA and IL-1 beta to form a plasmid (Q47738) which is then used a vaccine. NB: Sequence is difficult to read in the original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant plasmid for high immunogenity virus recombined haemagglutinin gene, hepatitis B core g
                                                      specification.
Sequence 208 AA;
                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
core / PV-1 / IL-1 Fusion.
core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
                                                                                                                                                                                                                                                                                         /label= PV-1
20..25
/label= IL-1
                                                                                                                                                                                                                                                                  26..208
/label=
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                   HBC
                                                                                                                                                                                                  LTD
 Score
Pred.
7; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1336; DB 8;
Pred. No. 2.72e-98;
6; Mismatches 3
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A
re 1337; DB 8; L
d. No. 2.24e-98;
Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 196;

    contains
    gene of vaccinia

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RESULT
ID RA
AC DT 16
DE H6
DE H6
KW H6
OS H6
PN J
PP 22
PR 24
PA (17
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Best Local S
Matches 17
16-FEB-1994 (first entry)
Hepatitis B core protein.
Hepatitis B; core; HBC; PV-1
Hepatitis B Virus.
J05192170-A.
J05192170-A.
J03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS LT
WPI; 93-277479/35.
                                                                                                                                                                                                                                      R40805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA used in prevention of infections by hepatitis virus B - comprises structural gene of hepatitis virus adr B surface antigen coding gene and at least 1 virus core antigen structural gene. Disclosure; Fig 3: 13pp; Japanese.

The sequence is that of hepatitis virus core antigen (HBcAg). It can be used as a vaccine for the prevention of infections by hepatitis B virus (HBV) and also in the diagnosis of early stages of HBV infection. See also P40310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1984,
19-OCT-1982; 183432.
19-OCT-1982; JP-183432.
(TAKE ) TAKEDA CHEMICAL IND KK.
WPI; 84-143231/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis virus core antigen.
HBCAg; vaccine; diagnosis; HBV
Hepatitis b virus.
J59074985-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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P40311 standard; Protein; 183
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                                                                                                                                                                                                                                                                   standard; Protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
175; Conse
                                                                                                                                                                                                                                                                                                                                                               183
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llarity 95.6%;
Conservative
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                                                                                                                                                                     PV-1;
                             CTD
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Pred. No. 3.99e-98;
5; Mismatches 3
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                                                                                                                                                                     beta; interleukin;
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Matches 17
                                                                                                                                                                                                                                                                                          Recombinant plasmid for high immunogenity virus - contains recombined haemagglutinin gene, hepatitis B core gene of vaccinia virus and exotic genes Disclosure; Fig 6; 12pp; Japanese.

The hepatitis B core gene is recombined with pv-1 DNA and IL-1 beta to form a plasmid (047738) which is then used to proactine. NB: Sequence is difficult to read in the original
                                                                                                                                                                                                                                                                  specification.
Sequence 183 AA;
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181
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llarity 95.6%;
Conservative
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Pred. No. 3.99e-98;
5; Mismatches 3
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##cross references ##cross references ##ccession S52334 ##molecule_type DN ##cross references	##residues_type DNA ##residues_tour ##cross-references; ##cross-references; ##cross-references; ##cross-references; ##cross-references; #authors Lai, M.E #submission submittee #accession S53191 ##molecule_type DNA ##residues 1-2: ##cross-references; ##cross-referenc	ACCESSIONS REFERENCE #authors #submission #description #accession	RESULT 1 ENTRY TITLE ALTERNATE_NAMES CONTAINS ORGANISM #Variety DATE
##COSS-references EMBL:X85313; NID:g736194; PID:g736196 ##cross-references EMBL:X85313; NID:g736194; PID:g736196 ##coss-references EMBL:X85313; NID:g736194; PID:g736196	##molecule_type DNA ##molecule_type DNA ##residues 1-212 ##label PLU ##cross references EMBL:235716; NID:g527435; PID:g527437 ##cross references EMBL:235716; NID:g527435; PID:g527437 ##cross references subtype ayw4, isolate hb321 NCE	S47405; S53191; S53209; S53234; S53264; S53249; S53262; S53277; A03711 S47404 Plucienniczak, A. submitted to the EMBL Data Library, August 1994 Molecular cloning and sequencing of two complete genomes of polish isolates of human hepatitis B virus. S47405	NKVLAH #type complete e antigen precursor / core antigen - hepatitis B virus (subtype ayw4, isolate hb321 and others) HBe antigen precursor / HBC antigen; pre-C/C antigen core antigen; e antigen #formal_name hepatitis B virus, HBV subtype ayw4, isolate hb321; isolate patient Ferracuti'83; isolate patient Castag'83; isolate patient Sanna'84; isolate patient Licheri-1'85; isolate patient Flore-1'86; isolate patient Licheri'83 18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change 10-Oct-1997

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CONTAINS ORGANISM
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Best Local Similarity 99.5%;
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30-178
179-212
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#accession S53249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #title Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.
#cross-references_MUID:81012091
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##residues 1-212 ##label LA6
##residues 1-212 ##label LA6
##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
cession $53277...
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##cross-references EMBL:X85317; NID:g736211; PID:g736214
##soperimental_source patient Glordo-2'86
##experimental_source patient Glordo-2'86
##enote due to a stop codon between the alternative initiators
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##cross-references GB:J02203; NID
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                                                                                                   S53211 #type complete
e antigen precursor / core antigen - hepatitis B virus
(isolate patient Castag-1'85 and others)
HBc antigen; HBe antigen precursor / HBc antigen; pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galibert, F.; Mandart, E.;
#formal_name hepatitis B virus, HBV
isolate patient Castag-1'85; isolate patient Ferracuti-1'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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                                                             core antigen; e antigen
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                                                                                    antigen
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#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #stat
predicted #label ECP
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Pred. No. 1.92e-206;
1; Mismatches 0;
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##cross-references EMBL:X85291; NID:g736117; PID:g736119
##experimental_source isolate patient Castag-1'85
cession S53197
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##cross-references EMBL:X85284; NID:g736095; PID:g736098
##cxperimental_source isolate patient Ferracuti-1'89
##enote due to a stop codon between the alternative
##cross-references EMBL:X72702; NID:g288927: PID:g288930
##experimental_source subtype ayw, patient C1000
##note due to a stop codon between the alternative
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l Similarity 98.9%;
182; Conservative
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$53112
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                                                                                                                 Gerok, W.; Rasenack, J.
submitted to the EMBL Data Library, March 1993
Identification and sequence analysis of hepatitis
in immunological negative infection.
                                                                                                                                                                                                                                                    #formal_name hepatitis B virus, HBV
subtype ayw, patient C1000
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-sep-1997
                                                                                                                                                                                                                                                                                                                                                       e antigen precursor / core antigen - (subtype ayw, patient C1000)
HBe antigen precursor / HBc antigen;
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##experimental_source isolate patient Castaa-2'87
due to a stop codon between the alternative initiatiors
the e antigen precursor cannot be produced
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S HBe antigen precursor / HBc antigen; precursor antigen; e antigen

#formal_name hepatitis B virus, HBV

subtype ayw, patient CI

20-Feb-1995 #sequence_revision 20-Feb-1908-Sep-1997
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Sequence analysis of HBV genomes isolated from
HBsAg negative chronic liver disease.
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#formal_name hepatitis B virus,
isolate patient Licheri-2'87
08-Jul-1995 #sequence_revision
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Licheri-2'87)
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##cross references EMBL:X85314; NID:g736201; PID:g736204
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##note the e antigen precursor cannot be produced
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           h 46.0%; Score 1370; DB 2; Similarity 98.9%; Pred. No. 1.39e-205; 182; Conservative · · 1; Mismatches 1;
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S53216
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e antigen precursor / core antigen -
(isolate patient Castag'3)
HBe antigen precursor / HBc antigen;
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$5311
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#formal_name hepatitis B virus, HBV
isolate patient Castay'3
08-Jul-1995 #sequence_revision 03-Au
                                                                                                                                                                                   alternative
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#product e antigen #status predicted #label EAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
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to the EMBL
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                                                                                                                                                                                 initiators; core protein
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                                                                      #molecular-weight 24363
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Pred. No. 1.39e-205;
3; Mismatches 0;
        1;
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Data Library, March 1995
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                                     Length 212;
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Local Similarity 98.9%;
hes 182; Conservative
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S53163
e antig
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core antigen; e antigen
formal_name hepatitits B virus, HBV
isolate patient Licheri-3'90
08-Jul-1995 #sequence_revision 03-Aug-1995
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e anti
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP
#length 212 #molecular-weight 24366 #checksum 446
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antigen
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  (isolate patient Licheri-3'90)
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precursor / core
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to the EMBL
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Pred. No. 1.39e-205;

    Mismatches

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Data
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Library,
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                             ##residues 1-212 ##label LAI
##cross-references EMBL:X65257; N
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              ##experimental_source subtype ayw, patient
                                                     ##molecule_type
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Similarity 98.9%;
182; Conservative
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S HBe antigen precursor / HBc antigen; precore antigen; e antigen

#formal_name hepatitis B virus, HBV

subtype ayw, patient C
20-Feb-1995 #sequence_revision 20-Feb-1
08-Sep-1997
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Sequence analysis of HBV genomes isolated from
HBSAg negative chronic liver disease.
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#formal_name hepatitis B virus, HBV
isolate patient Vittorina'92
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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Pred. No. 2.07e-205;
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                               NID:g59429; PID:g59431
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##experimental_source isolate patient Chighine-2'86
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Pred. No. 2.07e-205;
2; Mismatches 1;
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Pred. No. 2.07e-205;
3; Mismatches 0;
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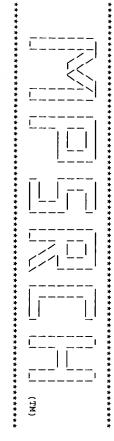
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##cross-reterences EMBL:X85285; NID:g736099; PID:g736100
##cross-reterences EMBL:X85285 patient Ferracuti-2'90
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isolate patient Ferracuti-2'90
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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                                                                                                                                                                                                                                                                               ##molecule_type DNA
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submitted t
S53223
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HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen
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                                                                                                                                                                                                                                                                                                                                                                                                       #formal_name hepatitis B virus, HBV
isolate patient Giordo 84
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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                                    #length
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to the EMBL Data Library, March 1995
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                                 #molecular-weight 24376
 Score 1366;
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Pred. No. 6.81e-205;
3; Mismatches 1;
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Best Local Similarity 98.4%;
Matches 180; Conservative
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##cross-references EMBL:x85275; NID:g736057; PID:g736060
##note due to a stop codon between the alternative initiations
the e antigen precursor cannot be produced
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                                                             SQC 183
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#superfamily hepatitis B virus core antigen
core protein
#length 183 #molecular-weight 21088 #checksum 1849
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HBC antigen
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S53112
Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri,
submitted to the EMBL Data Library, March 1995
S53169
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#formal_name hepatitis B virus, HBV
isolate patient Muresu'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                    Score 1364; DB 2;
Pred. No. 1.51e-204;
2; Mismatches 1;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 12:48:53 1999; MasPar time 12.80 Seconds 874.642 Million cell updates/sec

Scoring table:

Title:

Description: Perfect Score: Sequence: >US38183-1-38183 (1-396) from us38183-1-38183.pep 2977 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 396

РАМ 150 Gap 11

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

77977 seqs, 28268293 residues

Database: swiss-prot37 1:swissprot

Statistics: Mean 48.173; Variance 102.286; scale 0.471

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1374 1358 1349 13349 13349 1334 1332 1332 1332 1332 1331 1313 1305 1305 1305 1305 229 229 229 229 229 229 229 229 229 22	Score
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U1 SMALL NUCLEAR RIBON	PUTATIVE PRE-MRNA SPLI	PEROXIDASE / CATALASE	SPLICING FACTOR, ARGIN	SPERM PROTAMINE P1 (CY	SPERM PROTAMINE P1 (CY	PEPTIDYLPROLYL ISOMERA	PUTATIVE PRE-MRNA SPLI	PROTAMINE.	SPERM-SPECIFIC PROTEIN	SPERM HISTONE (PROTAMI	SPERM PROTAMINE P1.	SPERM PROTAMINE P1.	SPERM PROTAMINE P1.	SON PROTEIN (SON3).	REGULATORY PROTEIN E2.	SPERMATID-SPECIFIC PRO	SPERM PROTAMINE P1.	SPERMATID-SPECIFIC PRO	HYPOTHETICAL 24.0 KD P	PUTATIVE SPLICING FACT	CHOLESTERYL ESTER TRAN
2.69e-02	1.12e-02	1.50e-02	8.35e-03	1.12e-02	1.12e-02	6.21e-03	6.21e-03	4.62e-03	4.62e-03	6.21e-03	1.88e-03	1.88e-03	2.54e-03	3.00e-04	3.00e-04	4.09e-04	3.00e-04	6.30e-05	1.33e-06	4.83e-08	7.05e-13

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01-MAR-1992
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REPEAT 183 190
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P24023;
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PIR; A34773; NKVLA1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEPATITIS B VIRUS (STRAIN VIRUSES;
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                                                                                                                                                                                                                                                                                                                                                                                 . Similarity
179; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 AA;
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198
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larity 95.2%;
Conservative
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                                                               211
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21, LAST SEQUENCE UI
21, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24208 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHA1).
HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                                                                                                                                                                                                                                                                                                              Score 1358; DB 1;
Pred. No. 2.35e-233;
5; Mismatches 4;
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pre-C region
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RESULT
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Best Local S
Matches 17
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P17392;
01-AUG-1990
.01-AUG-1990
.01-FEB-1991
SEQUENCE FROM N.A.

MEDLINE; 89010694.

MIYAKAWA Y., TSUDA F., SAKUGAWA H., SASTRO
MIYAKAWA Y., MAYUMI M.;

"Typing hepatitis B virus by homology in
comparison of surface antigen subtypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J02202; G329638; -.
EMBL; A08967; G411874; -.
PIR; B93217; NKVLAA;
PFAM; PF00906; Hepatitis_core;
CORE PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEADBETTER G., MURRAY K.; "Hepatitis B virus genes and their expression NATURE 282:575-579(1979).
                                                                                                                                                                                             CORE ANTIGEN.
HEPATITIS B V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 81012115.
PASEK M., GOTO T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORE ANTIGEN
                                                                                                                                                                         VIRUSES; RETROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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l similarity 96.7%;
177; Conservative
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170
183 A
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(REL.
                                                                                                                                                                                             VIRUS (SUBTYPE ADW / STRAIN OKINAWA/PODW282)
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(REL.
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                                                                                                                                                                       VIRUSES;
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                                                                                                                                                                                                                                            15, CREATED)
15, LAST SEQUENCE UP
17, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01, CREATED)
01, LAST SEQUENCE UPDATE)
12, LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
177
21042 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUBTYPE ADYW).
/IRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GILBERT
                                                                                                                                                                         HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Pred. No. 1.41e-231;
5; Mismatches 1;
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                                                                          SASTROSOEWIGNJO R.I., IMAI
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Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P03150; p03151;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDAT
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SEQUENCE
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  MEDLINE: 89010694.
OKAMOTO H., TSUDA F.,
MIYAKAWA Y., MAYUMI M
                                                                                                                                                                                                                                                                                                                                                 ONO Y., ONDA H., SASADA R., IGARASHI K., S
"The complete nucleotide sequences of the
DNA; subtype adr and adw.";
NUCLEIC ACIDS RES. 11:1747-1757(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADR4), AND HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN INDONESIA/PIDW420). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORA_HPBV4
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                                                                                                                                                                                                              FUJIYAMA A., MIYANOHARA
MATSUBARA K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B28925; NKVLJ2
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                                                                      STRAIN-ADW
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                     "Cloning and
                                                                                                                                                                                                                                                       MEDLINE; 83246570
                                                                                                                                                                                                                                                                                    STRAIN-ADR4
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 83168919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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176; Conser
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170
183
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                                                                                                                                          11:4601-4610(1983)
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                             SAKUGAWA
                                                                                                                                                                                                                                   Α.
                                                                                                                                                                                                                               NOZAKI C., YONEYAMA T., OHTOMO N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1336;
Pred. No. 5.
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No. 5.22e-229;
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Best Local (
                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean.Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE: 89010694.
OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO R
OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO R
MIYAKAWA Y., MAYUMI M.;
"Typing hepatitis B virus by homology in nucleotide
comparison of surface antigen subtypes.";
J. GEN. VIROL. 69:2575-2583(1988).
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EMBL; X01587; G59407; -
EMBL; D00331; -; NOT_ANNOTATED_CDS.
PIR; A93480; NKVLA5.
PIR; B93460; NKVLA4.
PIR; C28925; NKVLJ3.
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J. GEN. VIROL. 69:2575-2583(1988).
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Pred. No. 1.30e-228;
5; Mismatches 3;
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PIR; C93460; NKVLA6
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"The complete nuclectide sequences of the
DNA; subtype adr and adw ";
NUCLEIC ACIDS RES. 11:1747-1757(1983).
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                                                                                                                                                                              Match 44.4%;
Local Similarity 96.2%;
les 178; Conservative
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Local Similarity 96.28;
es 176; Conservati
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                                                                                                               1 MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL 60
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172
185 AA;
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. 01, LAST SEQUENCE. 12, LAST ANNOTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169
177
                                                                                                                                                                                                                                                                     21394 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                                                                                                            Score 1321;
Pred. No. 4.
4; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADW)
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ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1322; DB 1;
Pred. No. 3.03e-226;
3; Mismatches 4;
                                                                                                                                                                                                                                                                       791E0381 CRC32;
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                                                                                                                                                                              Mismatches
                                                                                                                                                                       21; DB 1; Le.
4.78e-226;
hes 1;
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d hepatitis B
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01-NOV-1995 (REL. 3
01-NOV-1995 (REL. 3
01-NOV-1995 (REL. 3
CORE ANTIGEN.
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P29178;
P1-DEC-1992
01-DEC-1992
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01-DEC-1992
                                                                                                                                                                                                                                                                                             HEPATITIS
VIRUSES; F
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MEDILINE; 90169850.

BHAT R.A., ULRICH P.P., VYAS G.N.;

"Molecular characterization of a new variant of hepatitis:
a persistently infected homosexual man.";

HEPATOLOGY 11:271-276(1990).
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REPEAT
                          "Identification of a new hepatitis B virus that expresses HBV surface antigen subtype J. GEN. VIROL. 74:1627-1632(1993).
                                                                                                                               NAUMANN H., SCHAEFER GERLICH W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORA_HPBVT
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PFAM; PF00906; Hepatitis_core;

CORE PROTEIN; REPEAT.
                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).
RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
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LAST ANNOTATION UPDAT
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                                                                                                                                                                 YOSHIDA C.F.T.,
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HEPADNAVIRIDAE; OR
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ANNOTATION UPDATE)
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Pred. No. 1.15e-224;
9; Mismatches 3;
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PIR; A28885;
                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.
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                                  PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                                                                                                     "The complete nucleotide sequence of the virus isolated from a naturally infected J. GEN. VIROL. 69:1383-1389(1988).
                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE: 88258473.
                                                                                                                                                                                                                                                                                                                01-OCT-1989 (REL. 12, CREATED)
01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
CORE ANTIGEN.
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170
183 AA;
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ilarity 92.9%;
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195 2
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HEPADNAVIRIDAE; C
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Pred. No. 1.81e-224;
10; Mismatches 3;
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3 X 5 AA
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01-AUG-1990
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l Similarity 95.7%;
177; Conservative
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185 AA;
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Pred. No. 6.88e-223;
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                                                                                                                   SEQUENCE FROM N.A.
SPECIES=WOODCHUCK HEPATITIS VIRUS
MEDLINE; 88101359.
COHEN J.I., MILLER R.H., ROSENBLUB
                                                                                                                                                                                                                                                                                          "Nucleotide sequence of a cloned woodchuck hepatitis comparison with the hepatitis B virus sequence."; J. VIROL. 41:51-65(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES-WOODCHUCK HEPATITIS VIRUS
MEDLINE; 82216969.
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                                                                                                                                                                                                                                                                                                                                                                                           GALIBERT F., CHEN T.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIRUSES; RETROID
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                                                       "Sequence comparison of woodchuck hepatitis
                                                                                       PURCELL R.H.
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8 (INFECTIOUS CLONE) (WHV 8)
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Pred. No. 1.08e-222;
5; Mismatches 2;
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EMBL; M18752; G336140; -.
EMBL; M19183; G336145; -.
EMBL; J04514; G336149; -.
PIR; A03713; NKVLC.
PIR; C32397; NKVLCT.
PIR; C32397; NKVLC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORA_HPBGS
P03153;
21-JUL-1986
21-JUL-1986
01-JAN-1990
                                                                  "Nucleotide sequence of an infectious ground squirrel hepatitis virus."; J. VIROL. 51:367-375(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide sequence of a molecular clone of w hepatitis virus that is infectious in the natural host. PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
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                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 84267998.
                                                                                                                                                                                                                                                                                                                                                                    GROUND
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   This SWISS-PROT entry is copyright.
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larity 67.0%;
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Pred. No. 6.28e-151
25; Mismatches 32
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Query Match 31.3%;
Best Local Similarity 66.3%;
Matches 124; Conservative
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Best Local Similarity 68.1%;
Matches 128; Conservative
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE; 86062931.

KODAMA K., OGASAMARA N., YOSHIKAWA H., MURAKAMI S.;

Nucleotide sequence of a cloned woodchuck hepatitis virus genome:

Pucleotide sequence of a cloned woodchuck hepatitis virus genome:

evolutional relationship between hepadnaviruses.";

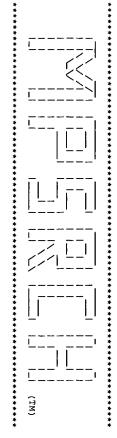
J. VIROL. 56:978-986(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORA_WHV8 P06433;
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SEQUENCE
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                                                                                                                                     EMBL; M11082; G336135; -. PIR; A03714; NKVLC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
                                                             SEQUENCE
                                                                                                        PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; K02715; G325401; -. PIR; A03715; NKVLS.
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VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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187 AA;
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Pred. No. 5.89e-150;
26; Mismatches 33;
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Pred. No. 3.77e-150;
22; Mismatches 32;
                                                             A1C354F3 CRC32;
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Search completed: Thu Dec 16 12:49:59 1999 Job time : 66 secs.

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Dec 16 12:50:17 1999; MasPar time 26.61 Seconds 812.364 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US38183-1-38183 (1-396) from us38183-1-38183.pep 2977 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 396

Scoring table: PAM 150 Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.585; Variance 101.482; scale 0.459

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16 17 18 19 20	110 111 113 114	V 4 70 7 80	Result No.
1366 1364 1363 1363	1370 1370 1369 1369 1368	1373 1373 1373 1373 1372	Score 1375 1374
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l Similarity 99.5%;
183; Conservative
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G (TREMBLREL.
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                                                                                                                                  HEPADNAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1374; DB 14;
Pred. No. 3.37e-231;
2; Mismatches 0;
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LAST SEQUENT ANNUAL AST ANNUAL ANNU
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Pred. No. 2.16e-231;
1; Mismatches 0;
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BANKS
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Best Local
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089437 PRELIMINARY:
089437; ORNOV-1996 (TREMBLREL. 01, CF)
01-NOV-1996 (TREMBLREL. 08, LF)
01-NOV-1998 (TREMBLREL. 08, LF)
X,_PREC AND C GENES (CASTAA 2)
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EMBL; X72702; G288930; -.
EMBL; X80925; E198084; -.
PFAM; PF00906; Hepatitis core;
SEQUENCE 212 AA; 24336 MW;
EMBL; X85289; G736113;
EMBL; X80925; E198085;
PFAM; PF00906; Hepatit;
SEQUENCE 183 AA; 21
                                                                                                                                      STRAIN=PATIENT CASTAA-2'87;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of hepatitis negative infection."; ARCH. VIROL. 133:385-396(1993).
                                      KARAYIANNIS P.;
SUBMITTED (SEP-1995) TO
                                                                                       SUBMITTED (DEC-1995) TO
                                                                                                          STRAIN-AYW;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                    HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
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SUBMITTED (DEC-1995)
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RASENACK J.;
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                                                           STRAIN-AYW,
                                                                                                  KARAYIANNIS P.;
                                                                                                                    SEQUENCE FROM
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                                                                   SEQUENCE FROM N.A.
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l Similarity 98.9%;
l82; Conservative
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 Hepatitis_core; AA; 21102 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1374; DB 14;
Pred. No. 3.37e-231;
2; Mismatches 0;
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LAST SEQUENCE UPDATE)
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01-NOV-1996 (TREMBI
01-NOV-1998 (TREMBI
PRE C/C ORF.
HEPATITIS B VIRUS.
VIRUSES; RETROID VI
                                                                                                                                                                                                      Q67876;
Q67876;
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01-NOV-1996
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STRAIN-PATIENT FERRACUTI-1'89;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA I
EMBL; X85284; G736098; -
EFAM; PF00906; Hepatitis core; 1.
SEQUENCE 183 AA; 21102 MW; BBE9AFBB CRC32;
SEQUENCE FROM N.A.
STRAIN-PATIENT CI, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRUSES;
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C GENES (FERRACUTI 1).
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larity 99.5%;
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Pred. No. 5.26e-231;
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Best Local Similarity
Matches 182; Conser
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01-JUL-1997 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
CORE ANTIGEN PRECURSOR.
HEPATITIS B VIRUS.
                   Q68066;
Q68066;
Q1-NOV-1996
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X, PREC AND
CORE
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O11884;
O1-JUL-1997
O1-JUL-1997
O1-NOV-1998
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SEQUENCE FROM N.A., RINAUDO J.S., KORBA SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ EMBL; U95551; G2182120; -.

PFAM: PF00906; Hepatitis_core: 1.
SEQUENCE 212 AA; 24360 MW; 73AC92DB CF
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EMBL; X65258; G59456; -.
PFAM; PF00906; Hepatitis_core;
SEQUENCE 212 AA; 24348 MW;
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1 Similarity 98.98;
182; Conservation
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                                    G (TREMBLREL. () (TREMBLREL. () (TREMBLREL. () C GENES (LICH
                                                                                                                              PRELIMINARY;
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llarity 98.9%;
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01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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Pred. No. 5.
2; Mismatc
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Pred. No. 8.20e-231;
2; Mismatches 0;
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d. No. 5.26e-231;
Mismatches 0;
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PRE-C/CORE.
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85315; G736207; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;
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STRAIN-PATIENT LICHERI-2'87;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85314; G736204; -.
PFAM: PF00906; Hepatitis_core; 1.
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Local Similarity 98.9%;
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                                                                                                         VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTIPSPRRRRSQSPRRRRSQSR 208
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                                                                                              VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
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(TREMBLREL.)
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            PRELIMINARY;
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AA; 21102 MW;
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LAST SEQUENCE UPDATE;
LAST ANNOTATION UPDATE;
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Pred. No. 1.99e-230;
            PRT;
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6F38AA3B CRC32;
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01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
PRE C/C ORF.
HEPATITIS B VIRUS.
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PRE-C/CORE.
HEPATITIS B
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01-NOV-1996
01-NOV-1996
01-NOV-1998
PRE-C/CORE.
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PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-PATIENT C, HBSAG POSITIV, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BA
                                                                                                                                                                                                                          EMBL; X65257; G59431; -. PFAM; PF00906; Hepatitis_core; SEQUENCE 212 AA; 24348 MW;
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                                                                                                                                                                                                                                                                                                                            VIRUSES;
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Local Similarity 98.9%;
hes 182; Conservation
209 ESQC 212
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                      VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 208
                                                                                    LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLIFGRETVIEYL 148
                                                                                                                                    GMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYRDALESPEHCSPHHTALRQAI 88
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                                                                       LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
                                                                                                                                                                        ch 46.0%;
l Similarity 98.4%;
181; Conservative
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RETROID VIRUSES;
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Pred. No. 1.99e-230;
1; Mismatches 1;
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LAST SEQUENCE ANNOTED
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Pred. No. 3.11e-230;
2; Mismatches 1;
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LAST SEQUENCE UPDATE)
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A6BD9DA1 CRC32;
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ANNOTATION UPDATE
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Q67984
Q67984;
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LAI M.E., MAZZOLENI A.P., PORRU A., BALEST
SUBMITIED (MAR-1995) TO EMBL/GENBANK/DDBJ
EMBL; X85296; G736139; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24308 MW; 69D87B53 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q68032;
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STRAIN-PATIENT VITTORINA'92;
STRAIN-PATIENT A.P., PORRU
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PRE-C/CORE.
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VIRUSES; RETROID VIRUSES;
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                                                                   SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 272
                                                                                                                                                            ch 46.0%;
l Similarity 98.4%;
181; Conservative
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182; Conser
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RETROID VIRUSES;
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98.9%;
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                                                                                                                                                            Score 1369; DB 14;
Pred. No. 3.11e-230;
3; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3.11e-230;
1; Mismatches 1;
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69D87B53 CRC32;
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K/DDBJ DATA BANKS
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Best Local Similarity
Matches 182; Conser
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Q68010;
Q1-NOV-1996
Q1-NOV-1996
                                                                             STRAIN-PATIENT GIORDO'84;
LAN M.E., MARZOLENI A.P., PORRU A., BALESTRIERI SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E EMBL; X85316; G736210; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24376 MW; 80F52D0F CRC32;
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANK
EMBL; X85285; G736100; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24292 MW; 04A4D12D CRC32;
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PRE-C/CORE.
HEPATITIS B VIRUS.
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1 Similarity 98.4%;
181; Conserva+4.--
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Pred. No. 4.
2; Mismatc
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LAST SEQUENCE UPDATE)
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LAST ANNOTATION UPDATE)
Score 1366; DB 14;
Pred. No. 1.18e-229;
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Search completed: Thu Dec 16 12:52:36 1999 Job time : 139 secs.

US3835-1-38183 MOIDPYKEFGATVELLSFLPSDEFPSVRÖLLDTASEIITRDGELLLQMDEGFPEHLLVDELQSLSMDIDP YKEFGATVELLSELPSDEFPSVRDLLDTASALYREALESPEHCSBHHTALRQAILCWGELMTLATWYGVN LEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTEGRETVIEYLVSFGVWIRTPPAYRPPNAPILSTLPE TTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRESQC1

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Thu Dec 16 12:57:17 1999; MasPar time 11.85 Seconds 445.188 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

>US3835-1-38183 (1-248) from us3835-1-38183.pep 1854 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 248

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Mean 33.490; Variance 173.849; scale 0.193

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length [DB	Ħ	Description	Pred. No.	
~	1375	74.2		32	W50242	Hepatitis B virus pre	9.89e-100	
2	1375	74.2		ະ	W50250	B virus	9.89e-100	
ω	1375	74.2	346	σ	R27473	S12/core protein.	9.89e-100	
4	1363	73.5		ب	P80959	Hepatitis B virus sub	9.52e-99	
ъ	1359	73.3		ະ	W50241	virus.	2.02e-98	
Ø	1358	73.2		ະ	W50251	B virus	2.44e-98	
7	1353	73.0		õ	W09044	Hepatitis B virus cor	6.28e-98	
œ	1349	72.8		1	R05635	Hepatitis B antigen.	1.33e-97	
9	1349	72.8		v	P00041	Sequence of core anti	1.33e-97	
10	1344	72.5		õ	W09048	Plasmid pHBV DN AA en	3.43e-97	
11	1338	72.2		ψ	P00004	Sequence of core anti	1.06e-96	ï
12	1336	72.1		œ	R40806	Hepatitis B core / PV	1.55e-96	
13	1337	72.1		œ	R40808	Hepatitis B core / PV	1.28e-96	
14	1334	72.0		4	P40311	Hepatitis virus core	2.26e-96	
15	1334	72.0		œ	R40805	Hepatitis B core prot	2.26e-96	
16	1334	72.0		Ü	R68868	Hepatitis B virus pol	2.26e-96	

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                                                                                                                                                             This polypepide comprises the hepatitis B virus (HBV) 25 kDa (p25) protein that is encoded by the full-length HBV precore gene. Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsids along with the p21 core protein (see W50251), which is the usual nucleocapsid component, and thereby render the nucleocapsids of the precore proteins, or certain variants of them, capression of the precore proteins, or certain variants of them, eagression of the precore proteins, or certain variants of them, inhibitory proteins include p25, p22 (see W50241), Met-p22 (see W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het recombinant methods using claimed expression vectors and host cells. They can be provided expension vectors and host cells. They can be provided expension vectors and host construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.
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Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1998.
03-SEP-1997; U15500.
03-SEP-1996; US-025370.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, Wands JR;
WPI; 98-193325/17.
                                                                                                                                                construct that directs overexpression of an target cells is used for the gene therapy of Sequence 212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding proteins which can be incorporated with wild type nucleocapsid subunit(s) into a viral nucleocapsid - useful for inhibition of viral replication, especially hepatitis B virus claim 15; Page 35; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatocyte; liver; p25 protein.
Hepatitis B virus.
W09809649-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1998 (first entry)
Hepatitis B virus precore p25 polypeptide.
Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W50250 standard; Protein; 212 AA
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                                                                                              Similarity
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99.5%;
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99.5%;
                                                                                           Score 1375; DB 32;
Pred. No. 9.89e-100;
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                                                                                     DR N-ESDB; (29105.)

PY Vaccine comprises recombinant, attenuated pox-virus - use for year vaccinating against viral infections such as rables, hepatitis B, PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

The sequence given is encoded by an expression cassette which comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/CC core) which is precisely linked to the I3L promoter derived from CC vaccinia virus. This DNA sequence was linked to the S1 and S2 core) which is precisely linked to the I3L promoter derived from CC sequences and this fragment was used in the construction of a NYVAC recombinant expressing the HBV gene. Other HBV genes were also used in the construction. These were HBV M protein (small pre-S antigen, spsAg) and HBV L (large pre-S antigen, 1psAg). Each of these gene sequences were inserted individually into three different sites of CC vaccinia virus which has been modified by deletion of six non-essential regions of the genome encoding known or potential virulence factors. The deletion loci were engineered as recipient loci for the insertion of the thetae inserted sequences ensured consecuria genome and would cause unviable vaccinia virus. See also
Query Match
Best Local s
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ULT 3
R27473 standard; Protein; 3
R27473; (first entry)
S12/core protein.
Hepatitis B virus; HBV; M p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1992.
09-MAR-1992; U01906.
07-MAR-1991; US-666056.
11-JUN-1991; US-713967.
06-MAR-1992; US-847951.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (VIRO-) VIROGENETICS CORP.

Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GI
Limbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus
Riviere M, Tartaglia J, Taylor J;

WPI; 92-331718/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg; vaccinia virus; I3L; promoter; NYVAC; recombinant; HBV L; vaccinie virus; virulence factor s1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor
                                                                              Q35501-864.
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larity 99.5%;
Conservative
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164..346
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/label s
109..163
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Score
Pred.
1; M
re 1375; DB 5; I
1. No. 9.89e-100;
Mismatches 0;
                              Length 346;
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Best Local S
Matches 18
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07-DEC-1987; US-106538.
07-OCT-1987; US-939617.
(SCRI-) Scripps Clinic Res.
Thornton GB, Moriarty AM, Millich DR, McLachlan A.;
WPI: 88-163287/24.
New conjugates and fusion proteins of immunogenic polypepytide and hepatitis B core antigen and T cell stimulating polypeptide coresp. to core antigen, useful in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; p; English.

This sequence contains the T cell stimulating epitopes, amino acid residue 1-55 and 70-140. It is believed that the regions 1-44 and 70-140 do not contain determinants that suppress T cell activation. Polypeptides essentially consisting of 15 to 55 amino acids corresponding to the above mentioned HBV regions are T cell stimulating. Coupling a polypeptide immunogen to such sequences, e.g. by using a bifunctional reagent which forms a disulphide link, improves its immunogenicity. These are useful in vaccines and can be therapeutically to improve T cell response to HBCAg in infected
F 5
W50241 standard;
W50241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1990 (first entry)
Hepatitis B virus subtype ayw. core protein.
Conjugate; fusion protein; hepatitis B core protein; HBV subtype ayw.;
T cell stimulating polypeptide; vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P80959;
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See also P80896-P80898 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
EP-271302-A.
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                                                                                                                                                                                                                                                                                                                                                                 CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTF-GRETVIEYL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                             Protein; 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%;
99.5%;
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Pred. No. 9.52e-99;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 184;
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ID WE
AC WE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT DNA encoding proteins which can be incorporated with wild type proteins which can be incorporated with wild type protein submit(s) into a viral nucleocapsid - useful for protein this polypeptide comprises the hepatitis B virus Claim 9; Page 34-35; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22) crocein that is produced by elimination of the 19-amino acid leader certain that is produced by elimination of the 19-amino acid leader certain the 25 kDa full-length HBV precore protein (see W50250). Evidence is provided that HBV replication is inhibited in ct the presence of high levels of HBV precore or precore-related croce proteins. These proteins can be incorporated into HBV nucleocapsids component, and thereby render the nucleocapsids concleocapsid concleocapsid concleocapsid strip HBV pregenomic RNA. Thus, over-cappression of the precore proteins, or certain variants of them, cleaked to transdomanant inhibition of HBV replication. Suitable consistency proteins include p25 (see W50237), p22, Met-p22 (see W50242), p18 (see W50238), Met-p18 (see W502437) and Met-p18 HHet (see W50242), p18 (see W50238), Met-p18 (see W50244-49) may be consistent methods using claimed corporate and host cells. They can be provided exogenously continued that directs overcexpression contents of the protein in target cells is used for the gene contents of HBV infection.
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Best Local S
Matches 18
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12-MAR-1998.
03-SEP-1997; U15500.
03-SEP-1996; US-0253
                                    w50251 standard; Protein; 183 AA.
w50251;
28-SEP1998 (first entry)
Heparitis B virus p21 core protein.
viral replication; inhibitor; HBV; nucleocapsid;
hepartocyte; liver; p21; core protein.
Heparitis B virus.
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Melegari M, Scaglioni PP, Wands
WPI; 98-193325/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%;
11 Similarity 98.4%;
181; Conservation
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    Location/Qualifiers
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Pred. No. 2.02e-98;
2; Mismatches 1;
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This is the 21 kDa (p21) protein of hepatitis B virus (HBV) that assembled into a 180 kSa subunit nucleocapsid Structure that promotes viral replication. Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsids along with the p21 core protein and thereby render the nucleocapsids deficient in encapsidating HBV pregenomic RNA. Thus, over-expression of the precore proteins or certain variants of them, leads to transdominant inhibition of HBV replication. Suitable inhibitory proteins include p25 (see w5023), p22 (see w50241), Met-p22 (see w50242), p18 (see w50235), Met-p18 (see w50237) and Met-p22 (see w50238). These proteins can be produced by recombinant methods using claimed expression vectors and host cells, and can be provided exogenously to target cells for use in inhibiting HBV replication. Alternatively, a nucleic acid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                               Hepatitis B virus core protein.
Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus;
ground squirrel hepatitis B virus; duck hepatitis B virus;
                                                                                                                                                                                                                                                                W09044 standard: Protein: 183
W09044:
11-APR-1997 (first entry)
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Melegari M. Scaglioni PP,
WPI: 98-193325/17.
                     misc_difference
                                                                                    misc_difference
                                                                                                                                                      misc_difference
                                                                                                                                                                                 Hepatitis B virus
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12-MAR-1998.
03-SEP-1997; U15500.
03-SEP-1996; US-025370.
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                                                                                                                                                                                                   protein; replication; antiviral;
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181; Consen
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larity 98.9%;
Conservative
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                    /note= "C-terminus of
acid position between
polypeptides of the in
171...180
                                                                                  /note= "C-terminus of core protein is at any acid position between 71-180 in mutant polypeptides of the invention (Claim 23)" 81..180
                                                                                                                                                      71..180
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                                                                                                                                                                ocation/Qualifiers
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Pred.
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. No. 2.44e-98;
Mismatches 1;
      of.
                                   invention
                                   core protein is at any 81 and 180 in mutant nvention (Claim 5)"
      core
                                                                                                                                                                                                 gene therapy.
   protein is at any
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Best Local s
Matches 18
Hepatitis B antigen.
Hepatitis B virus; va
Synthetic.
EP-374869-A.
27-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis B virus (HBV) or other hepadnavirus creates a mutant polypeptide capable of reducing replication of the wild-type virus by a dominant negative mechanism. The inhibitory effect is species-specific and is achieved by deletion of a few C-terminal amino acids from the core protein, and/or by joining the core protein to a hepadnavirus surface protein (see also W09045), creating a core-surface fusion. Such mutant polypeptides (see also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-1997.
20-JUN-1996;
20-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New method for inhibiting the replication of hepadnaviruses -
comprises introducing a mutant polypeptide with a mutated core
protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                                        30-OCT-1990
                                                                                    R05635 standard;
R05635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 55-56; 83pp; English. Alteration of the C-terminus of the core protein (W09044) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melegari M, Scaglioni WPI; 97-087176/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-1990, US-017814.
20-JUN-1995; US-017814.
(GEHO) GEN HOSPITAL CORP.
GEAGLIONI PP,
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Similarity 98.9%;
181; Conservative
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                                                                     (first entry)
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polypeptides of
174..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminus of core protein is at an acid position between 174 and 180 in mutant polypeptides of the invention (Claim 26)" 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amino acid residues 172-183,
are deleted from the core protein in
polypeptides of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               position 178 in mutant polypeptides invention (Claim 7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminus of core protein is at amino acid
position 178 in mutant polypeptides of the
invention (Claim 7)"
                                                                                                 protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "C-terminus of core protein
                                            HBV;
                                                                                                                                                                                                                                                                                                                                                                                    Score 1353; DB 20;
Pred. No. 6.28e-98;
0; Mismatches 2;
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1 (Claim
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Matches 1
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Matches
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21-DEC-1979;
22-DEC-1978;
                                                                                                   Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Example; Figs 3-4; 43pp; English. Human serum from a single HBSAg positive, HBBAg positive donor (serotype adym) was used to prep. a DNA-contg. pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of core antigen.
Hepatitis B virus; antigen;
Hepatitis B virus.
EP--13828-A.
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01-NOV-1979;
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Murray K, Schaller HE;
WPI; 90-195067/26.
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22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039
01-NOV-1979; GB-037910
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  1 Similarity
177; Conser
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177; Conse
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8; GB-049907.
8; GB-050039.
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GB-049907.
GB-050039.
GB-037910.
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llarity 96.7%;
Conservative
72.8%;
larity 96.7%;
Conservative
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Pred. No. 1.33e-97;
5; Mismatches 1
Score
Pred.
5; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; diagnosis; vaccine.
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e 1349; DB 5;
. No. 1.33e-97;
Mismatches 1;
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                                                                                                                                                     Disclosure; Page 46-48; 83pp; English.

Plasmid phBv DN AA carries an Insert (T49598) coding for a protein (See also W99048) comprising a hepatitis B virus (HBV) core protein (see calso W99044) fused in-frame at amino acid 179 with the HBV surface protein (see also W09045) at amino acid a mino acid 175 to the C (T49599) expresses the HBV core fused at amino acid 175 to the Surface protein at amino acid 112 (W09049). pHBV DN AA was at C least as potent an inhibitor of HBV replication as construct C PHBV DN (T49597); pHBV DN BB was less inhibitory than pHBV DN. C Vectors expressing hepadnavirus dominant negative core mutants can be utilised in the gene therapy of viral infections.
                                                                                                 Query Match
Best Local s
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                  W09700698-A1.
09-JAN-1997.
20-JUN-1996; U10602.
20-JUN-1995; US-017814.
(GEHO ) GEN HOSPITAL CORP.
MGLEGATI M, SCAGGLONI PP,
WPI; 97-087176/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid phBv DN AA encoded HBv dominant negative polypeptide. Plasmid phBv DN AA encoded HBv dominant negative polypeptide. Hepadnavirus; woodchuck hepatitis virus; hepatitis delta viru HBv; ground squirrel hepatitis B virus; duck hepatitis B viru core protein; replication; antiviral; gene therapy; phBv DN A Hepatitis B virus.
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W09048 standard;
W09048;
11-APR-1997 (fir
                                                                                                                                                                                                                                                                                                                                       N-PSDB; 749598.

New method for inhibiting the replication of hepadnaviruses - comprises introducing a mutant polypeptide with a mutated core protein or corresponding nucleic acid, for treating, e.g. hepatitis
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                                          MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
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                                                                                                ch 72.5%;
l similarity 100.0%;
179; Conservative
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/note= "positions 1-179 correspond
1-179 of HBV core protein"
180..397
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9-226 of HBV surface
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                                                                                              Score 1344; DB 20;
Pred. No. 3.43e-97;
0; Mismatches 0;
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DN AA.
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sfgvwirtppayrppnapilstlpettvvrrrgrsprrrtpsprrrrsqsprrrrsqsr

CWGELMTLATWYGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV

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Best Local S
Matches 17
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21-DEC-1979; 303017.
22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Claim 13; Page 40; 43pp; English. Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-cont, pellet which was labelled with 3H or 32p as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HBJO1/pBR322-Pst I dG: HBY-KPN I dC: Tetr AmpS HBV+.
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J05192170-A.
03-AUG-1993;
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS LTD
                                                                                                                              IT 12
R40806 standard; Protein;
R40806;
15-FEB-1994 (first entry)
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Murray K, Schaller HE;
WPI; 80-57268C/33.
                                                                                          Synthetic
Key
                                                                                                           Hepatitis B core / PV-1 fusion Hepatitis B; core; HBC; PV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; N00002
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l Similarity 96.2%;
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14..196
/label=
                                                                                         Location/Qualifiers
                                                                                                                                                   Protein; 196
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                                                                      PV-1
                                                   HBC
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Pred.
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Best Local S
Matches 17
                                                                                   Matches
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Best Local :
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Hepatitis
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Disclosure; Fig 7; 12pp; Japanese.
The hepatitis B core gene is recombined with PV-1 DNA and IL-1 beta to form a plasmid (Q47738) which is then used a vaccine. NB: Sequence is difficult to read in the original
                                                                                                                                                                                                 Recombinant plasmid for high immunogenity virus - contrecombined haemaggluttnin gene, hepatitis B core gene virus and exotic genes.

The hepatitis B core gene is recombined with pv-1 DNA and L-1 beta to form a plasmid (047738) which is then a vaccine. NB: Sequence is difficult to read in the or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IT 13
R40808 standard; Protein;
R40808;
R6-FEB-1994 (first entry.)
                                                                                                                                                                                                                                                                                                                                         (NISW ) NISSHIN OIL MILLS WPI; 93-277479/35. N-PSDB; Q47738.
                                                                                                                                                                                                                                                                                                                                                                                                J05192170-A.
03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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N-PSDB; Q47736.
                                                                                                                                                                specification.
Sequence 208
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    esqc 196
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l Similarity 95.1%;
l75; Conservative
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175; Conser
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8..19
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20..25
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26..208
/label= HBC
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HBC;
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                                                                             Score 1337;
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7; Mismatcl
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1. No. 1.55e-96;
Mismatches 3;
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                                                                                               DB 8;
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Hepatitis virus core antigen.
HBCAG; vaccine; diagnos18; HBV in
HBCAG; vaccine; diagnos18; HBV in
HEPATITIS b virus.
J59074985-A.
J59074985-A.
J59074985-A.
J9074985-A.
J907498-A.
J90748-A.
J907
                                            03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS LTD.
WPI; 93-277479/35.
N-PSDB; Q47735.
Recombinant plasmid for high immunogenity virus - recombined haemagglutinin gene, hepatitis B core g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA used in prevention of infections by hepatitis virus B comprises structural gene of hepatitis virus adr B surface antigen coding gene and at least 1 virus core antigen structural gene. Disclosure; Fig 3: 13pp; Japanese.

The sequence is that of hepatitis virus core antigen (HBCAg). It can be used as a vaccine for the prevention of infections by hepatitis B virus (HBV) and also in the diagnosis of early stages of HBV infection. See also P40310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-1994 (first entry)
Hepatitis B core protein.
Hepatitis B; core; HBC; PV-1;
Hepatitis B Virus.
J05192170-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 14
P40311 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R40805;
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l Similarity 95.6%;
175; Conservative
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exotic genes
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Pred. No. 2.26e-96;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-1 beta; interleukin; plasmid
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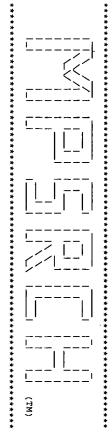
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Best Local
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                                                                                                                                                                                    Disclosure; Fig 6; 12pp; Japanese.
The hepatitis B core gene is recombined with pv-1 DNA
and IL-1 beta to form a plasmid (Q47738) which is then used to produce
a vaccine. NB: Sequence is difficult to read in the original
specification.
                                                                                                                                                                            Sequence
                                246
                                                                    126
                 181
                                                                   66
                                                                                                                                        y Match 72.0%;
Local Similarity 95.6%;
hes 175; Conservative
                                                                                                      SQC
               Sqc
                 183
                                                                                                                                                                             183 AA;
                                                                                                                                        Score 1334; DB 8; 1
Pred. No. 2.26e-96;
5; Mismatches 3;
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Search completed: Thu Dec 16 13:00:09 1999 Job time: 172 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:00:27 1999; MasPar time 12.64 Seconds 786.145 Million cell updates/sec

Description: Perfect Score: Sequence: >US3835-1-38183 (1-248) from us3835-1-38183.pep 1854 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 248

Scoring table: РАМ 150 Gap 11

Searched:

122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.523; Variance 119.912; scale 0.396

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
1375 1374 1374 1377 1377 1377 1370 1370 1370 1369 1369 1366 1366 1366 1366 1363 1363	Score
77744 77744 7773 7773 7773 7773 7773 77	Query Match
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NKVLAH S53207 S53211 S32204 S520750 S53270 S53276 S53272 S53272 S53225 S53163 S53225 S53163 S53225 S53169 S53226 S53226 S53227 S53226 S53226 S53226	ID
e antigen precursor / core antigen precursor e antigen precursor e antigen precursor / core antigen precursor e antigen precur	Description
4. 43e-199 6. 50e-199 6. 50e-199 6. 50e-199 9. 53e-199 3. 01e-198 3. 01e-198 4. 42e-198 4. 42e-198 4. 42e-198 4. 42e-198 1. 39e-197 4. 40e-197 4. 40e-197 4. 40e-197 6. 46e-197 6. 46e-197 1. 39e-196 1. 39e-196 1. 39e-196 1. 39e-196	Pred. No.

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NKVLJ2	\$53236	S25651	S53137	S53257	S53238	S53189	S53267	S53140	S53214	S53229	S53152	S53260	\$53232	S53181	NKVLA2	S53240	S53129	S53242	NKVLBH	S53281	NKVLAL
		n29	core antigen - hepati	e antigen precursor /	G.	,	,	,	core antigen - hepati	ecu	•	,	•	•	core antigen - hepati	ecurson	Q			eg	e antigen precursor /
.33e-	.36e-	-19	.34e-		2.02e-193	.02e-	.02e-	1.37e-19	9.37e-19	6.39e-19	.36e-	.38e-	1.38e-19	9.41e-19	.41e-		.37e-	e-19	.44e-	4.39e-19	2.99e-19

##residues ##residues ##residues ##cross references ##cression ##accession ##molecule_type DNA ##residues ##cross references	##residues 1-2; ##cross references: ##cross references: ##experimental_sour #accession \$53209 ##molecule_type DNA ##residues 1-2 ##cross references: ##cross references: ##cross references: ##accession \$53234	##residues ##residues 1-2 ##cross references: ##experimental_sour REFERENCE Lai, M.E #submission submittee #accession S53191	REFERENCE #authors #submission #description #accession	DATE ACCESSIONS	RESULT 1 ENTRY TITLE ALTERNATE_NAMES CONTAINS ORGANISM #VARIETY
##molecule_type DNA ##residues 1-212 ##label LA3 ##residues 1-212 ##label LA3 ##residues 1-212 ##label LA3 ##residues 1-212 ##label LA3 ##experimental_source isolate patient Sanna'84 cession S3364 ##molecule_type DNA ##residues 1-212 ##label LA4 ##residues 1-212 ##label LA4	##molecule_type DNA ##residues 1-212 ##label LAI ##coss-references EMBL:X85283; NID:g736088; PID:g736090 ##cross-references EMBL:X85283; NID:g736088; PID:g736090 ##cross-references EMBL:X85280; NID:g736114; PID:g736116 ##cross-references EMBL:X85290; NID:g736114; PID:g736116 ##cross-references EMBL:X85290; NID:g736114; PID:g736116 ##cross-references EMBL:X85290; NID:g736114; PID:g736116	##molecule_type DNA ##rosidues 1-212 ##label PLU ##rossi-references EMBL.235716; NID:g527435; PID:g527437 ##coss-references EMBL.235716; NID:g527435; PID:g527437 ##experimental_source subtype ayw4, isolate hb321 NCE S53112 Thors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A. bmission submitted to the EMBL Data Library, March 1995 cession S53191	S47404  Plucienniczak, A.  Submar, August 1994  Submar Library, August 1994  Submar Li	<pre>isoLate patient Castag'83; isolate patient Sanna'84; -isolate patient Licheri-1'85; isolate patient Flore-1'86; isoLate patient Licheri'83 18-Dec-1981 #sequence_revision O8-Nov-1996 #text_change 10-Oct-1997 \$47405; \$53191; \$53209; \$53234; \$53264; \$53249; \$53262; \$53277; A03711</pre>	NKVLAH *type complete e antigen precursor / core antigen - hepatitis B virus (subtype ayw4, isolate hb321 and others) HBe antigen precursor / HBC antigen; pre-C/C antigen core antigen; e antigen *formal_name hepatitis B virus, HBV subtype ayw4, isolate hb321; isolate patient Ferracuti'83;

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30-178
179-212
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#journal Nature (1979) 281:646-650
#title Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.
#cross-references_MUID:81012091
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##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
ression $53277
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##cross-references EMBL:x88306; NID:g736172; PID:g736174
##experimental_source isolate patient Flore-1'86
**exsion $53262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-212 ##label GAL
##cross-references GB:J02203; NID:g329640; PID:g329642
##experimental_source subtype ayw
                                                                                                                                                                                                                                                                                                                                                                          125
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                                                                                                                                                                                                                                                              209
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##note due to a stop codon between the alternative initiators
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                                                                                                                                                                                                                          ESQC 248
                                                                                                                                                                                                                                                            ESQC 212
                                                                                                                                                                                                                                                                                                                                  VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 74.2%;
Similarity 99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *superfamily hepatitis B virus core antigen alternative initiators; core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galibert, F.; Mandart, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A93214
               #formal_name hepatitis B virus, HBV isolate patient Castaa-2'87 08-Jul-1995 #sequence_revision 03-A
                                                                                           HBc antigen
                                                                                                        core antigen -
Castaa-2'87)
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08-Sep-1997
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP
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                                                                                                                                              #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #molecular-weight 24350 #checksum
                                                                                                                             hepatitis B virus (isolate patient
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Pred. No. 4.43e-199;
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                  03-Aug-1995
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##cross-references EMBL:X85289; NID:g736110; PID:g736113
##cross-references EMBL:X85289; NID:g736110; PID:g736113
##experimental_source isolate patient Castaa-2'87
due to a stop codon between the alternative initiatiors
the e antigen precursor cannot be produced
                                                                                                                                                                                                                                                                                             ##residues 30-212 ##label LAW
##cross-references EMBL:X85284; NID:g736095; PID:g736098
##cross-references EMBL:X85284; NID:g736095; PID:g736098
##experimental_source isolate patient Ferracuti-1/89
due to a stop codon between the alternative initiatiors
the e antigen precursor cannot be produced
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1-212 ##label LAI
##cross-references EMBL:X85291; NID:g736117; PID:g736119
##cross-references EMBL:X85291; NID:g736117; PID:g736119
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isolate patient Castag-1'85; isolate patient Ferracuti-1'89
isolate patient Castag-1'85; isolate patient Ferracuti-1'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
$53211; $53197
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e antigen precursor / core antigen - hepatitis B
(isolate patient Castag-1'85 and others)
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Pred. No. 9.53e-199;
1; Mismatches 0;
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##experimental_source subtype ayw, patient C1000
##note due to a stop codon between the alternative the e antigen precursor cannot be produced
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   LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
               LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 148
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HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen wirus, HBV subtype ayw, patient C1000

20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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Pred. No. 6.50e-199;
2; Mismatches 0;
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Sequence analysis of HBV genomes isolated
HBSAg negative chronic liver disease.
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HBe antigen precursor / HBc antigen;
core antigen; e antigen
#formal_name hepatitis B virus, HBV
core antigen
#formal_name hepatitis B virus,
isolate patient Licheri-2'87
08-Jul-1995 #sequence_revision (
                                                                    s53270 #type
core antigen - ]
Licheri-2'87)
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20-Feb-1995 #sequence_revision
08-Sep-1997
                                                          HBc antigen
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                                                                 #type complete
|en - hepatitis B
|2'87) >
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Pred. No. 9.53e-199;
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  03-Aug-1995
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Query Match 73.9%;
Best Local Similarity 98.9%;
Matches 182; Conservative
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##cross-references EMBL:X85293; NID:g736124; PID:g736126
##experimental_source isolate patient Castag'3
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##experimental_source isolate pattent Licheri-2'87
##note due to a stop codon between the alternative :
##note the e antigen precursor cannot be produced
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##residues 1-183 ##label LAI
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S53112
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(isolate patient Castag'3)
HBe antigen precursor / HBc antigen; pre-C/
core antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate patient Castag'3
08-Jul-1995 #sequence_revision 03-Aug-1995
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submitted t
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larity 98.4%;
Conservative
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alternative initiators; core protein
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#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #stat
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Pred. No. 3.01e-198;
3; Mismatches 0;
   Score 1370; DB 2; 1
Pred. No. 3.01e-198;
;2; Mismatches 1;
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Data Library, March 1995
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Data Library, March 1995
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##cross-references EMBL:X85315; NID:g736205; PID:g736207
##experimental_source isolate patient Licheri-3'90
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Local Similarity 98.98;
hes 182; Conservation
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S53163
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HBe antigen precursor / HBc antigen;
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP
#length 212 #molecular-weight 24366 #checksum 446
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08-Jul-1995 #sequence_revision 03-Aug-1995
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precursor / core antigen
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to the EMBL Data Library, Mar
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Pred. No. 3.01e-198;
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                                            ##cross-references EMBL:X65257; NID:g59429; PID:g59431
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                              ##experimental_source subtype ayw, patient
                                                                             ##molecule_type
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Similarity 98.9%;
182; Conservative
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*formal_name hepatitis B virus,

subtype ayw, patient C

20-Feb-1995 *sequence_revision 2
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e antigen precursor / core antigen -
(subtype ayw, patient C)
HBe antigen precursor / HBc antigen;
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
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HBe antigen precursor / HBc anti
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#formal_name hepatitis B virus, HBV
isolate patient Vittorina'92
08-Jul-1995_#sequence_revision 03-Aug-1995
                                                                                                                                Sequence analysis of HBV
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                                                                                                                                                                                Lai, M.E.; Mazzoleni,
                                                                                                             equence analysis of HBV genomes isolat HBsAg negative chronic liver disease.
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Pred. No. 4.42e-198;
1; Mismatches 1;
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125 LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 184
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                                 LCWGDLMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFKQLLWFHISCLTFGRETVIEYL 148
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Similarity 98.4%;
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Be antigen precursor / HBc antigen;
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predicted #label ECP
|th 212  #molecular-weight 24308 #checksum 655
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Pred. No. 4.42e-198;
2; Mismatches 1;
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HBe antigen precursor / HBC antigen;
core antigen; e antigen
#formal_name hepatitis B virus, HBV
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08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
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HBe antigen precursor / HBc antigen;
core antigen; e antigen
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                                             isolate patient Chighine-1'85
08-Jul-1995 #sequence_revision 03-Aug-1995
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                                                                            #formal_name hepatitis B virus, HBV
                             08-Sep-1997
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    predicted #label ECP
yth 212 #molecular-weight 24292 #checksum 593
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#product core antigen #status predicted #label CAG\
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Pred. No. 6.48e-198;
2; Mismatches 1;
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##cross-references EMBL:X85295; NID:g736134; PID:g736136
##experimental_source isolate patient Chighine-1'85
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Similarity 97.8%;
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submitted t
S53223
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HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen wirus, HBV

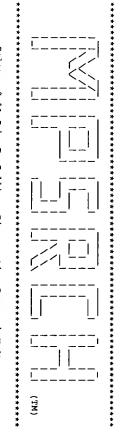
##formal_name hepatitis B virus, HBV

isolate patient Giordo'84

08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                                                                  *superfamily hepatitis B virus core antigen alternative initiators; core protein
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#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
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#product e antigen #status predicted #label EAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #statu
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1 212 #molecular-weight 24376
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1 212 #molecular-weight 24364 #checksum 1123
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Score 1366;
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Data Library, March 1995
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##experimental_source isolate patient Muresu'89
##enote due to a stop codon between the alternative initiatiors
the e antigen precursor cannot be produced
                                              246
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                                                                                                                                                                                                                                 Ch 73.6%; Score 1364; DB 2; Length 183; Similarity 98.4%; Pred. No. 3.00e-197; 180; Conservative 2; Mismatches 1; Indels
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core antigen - hepatitis B virus (isolate patient Muresu'89)
HBC antigen
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:01:46 1999; MasPar time 8.80 Seconds 796.747 Million cell updates/sec

Description: Perfect Score: >US3835-1-38183 (1-248) from us3835-1-38183.pep 1854 1 MDIDDYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 248

Sequence:

Searched: PAM 150 Gap 11 77977 seqs, 28268293 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot37 1:swissprot

Statistics: Mean 48.750; Variance 106.745; scale 0.457

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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185 1 CORA_HPBVW CORE 195 1 CORA_HPBVF CORE 212 1 CORA_HPBVT CORE 183 1 CORA_HPBVL CORE 185 1 CORA_HPBV2 CORE	185 1 CORA_HPBVW CORE 195 1 CORA_HPBVF CORE 212 1 CORA_HPBVT CORE 183 1 CORA_HPBVI CORE 185 1 CORA_HPBV2 CORE 214 1 CORA_HPBV9 CORE	185 1 CORA_HPBVW CORE 195 1 CORA_HPBVF CORE 212 1 CORA_HPBVF CORE 183 1 CORA_HPBV CORE 185 1 CORA_HPBV2 CORE 214 1 CORA_HPBV9 CORE 188 1 CORA_WHV1 CORE	185 1 CORA_HPBVW CORE 195 1 CORA_HPBVF CORE 212 1 CORA_HPBVT CORE 213 1 CORA_HPBVT CORE 183 1 CORA_HPBVZ CORE 185 1 CORA_HPBV2 CORE 214 1 CORA_HPBV2 CORE 214 1 CORA_HPBGS CORE 217 1 CORA_HPBGS CORE 217 1 CORA_HPBGS CORE 289 1 CETP_MESAU CHOLE 289 1 CETP_MESAU CHOLE 289 1 CETP_MESAU CHOLE 289 1 CETP_MACRA CHOLE 305 1 CORA_HPBBC CORE	Score 1374 1358 1349 1336 1334	Query Match 74.1 73.2 72.8 72.8 72.1	Length D 183 211 183 183 183		ID CORA_HPBVY CORA_HPBVA CORA_HPBVZ CORA_HPBVO CORA_HPBVO CORA_HPBVJ	1 H
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Query Match 74.1%; Score 1374; DB 1; Length 183; Best Local Similarity 100.0%; Pred. No. 6.54e-229;

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EMBL; V01460; G62278; ALT_INIT. EMBL; X02496; -; NOT_ANNOTATED_CDS. PIR; A03711; NKVLAH. PIR; A03712; NKVLAH. PFAM; PF00906; Hepatitis_core: 1. CORE PROTEIN; REPEAT. REPEAT 162 169 REPEAT 170 177 REPEAT 170 177 CONFLICT 33 33 T -> N (IN REF. 2). CONFLICT 80 80 A -> I (IN REF. 2). SEQUENCE 183 AA; 21116 MW; 2AE7417A CRC32;	SWISS- sen th thropea by no by no fied an ties re	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE; 81012091.  GALIBERT F., MANDART E., FITOUSSI F., TIOLLAIS P., CHARNAY P.;  "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  cloned in E. coll.";  NATURE 281:646-650(1979).  [2]  SEQUENCE FROM N.A. (CLONE PHB320).  MEDLINE; 85204397.  SIDTYPE BY VARIANT OF hepatitis B virus. DNA primary structure analysis.";  FEBS LETT. 185:208-212(1985).	LT 1 CORA_HPBVY STANDARD; PRT; 183 AA. p03146; p03146; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 21-JUL-1990 (REL. 14, LAST ANNOTATION UPDATE) CORE ANTIGEN. C. HEPATITIS B VIRUS (SUBTYPE AYW). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

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PIR; A34773; NKVLA1.
PFAM; PF00906; Hepatitis_core; 1.
CORE PROTEIN; REPEAT.
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179; Conser
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21, LAST SEQUENCE UPDATE)
21, LAST ANNOTATION UPDAT
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Pred. No. 7.60e-226;
5; Mismatches 4;
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EMBL; A08967; G411874; -.
PIR; B93217; NKVLAA.
PFAM; PF00906; Hepatitis_core; 1
CORE PROTEIN; REPEAT.
REPEAT 162 169
REPEAT 170 177
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21-JUL-1986
21-JUL-1986
01-OCT-1989
                                                                                                                                    CORA_HPBVO STANDARD; PRT; 1
p17392;
p1-390 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UP
01-FEB-1991 (REL. 17, LAST ANNOTATION
CORE ANTIGEN.
HEPATITIS B VIRUS (SUBTYPE ADW / STRAI
SEQUENCE FROM N.A.

MEDLINE; 89010694.

OKAMOTO H., TSUDA F., SAKUGAWA H., SASTRO
MIYAKAWA Y., MAYUMI M.;

"Typing hepatitis B virus by homology in
comparison of surface antigen subtypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PASEK M., GOTO T.,
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                                                                                                                      VIRUSES; RETROID
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"Hepatitis B virus genes and their expression
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Similarity 96.7%;
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(REL.
                                                                                                                       VIRUS (SUBTYPE ADW / STRAIN OKINAWA/PODW282).
TROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIF
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12, LAST ANNO
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                                                                                                                         HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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ANNOTATION
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Pred. No. 4.02e-224;
5; Mismatches 1;
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                                                     SASTROSOEWIGNJO R.I., IMAI M.,
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P03150; P03151;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
01-FEB-1991 (REL.)
MEDLINE; 89010694.
OKAMOTO H., TSUDA F.,
MIYAKAWA Y., MAYUMI M.
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                                                                                                                                                                                                     MEDLINE: 83168919.

ONO Y., ONDA H., SASADA R., IGARASHI K., 9
"The complete nucleotide sequences of the DNA; subtype adr and adw.";
                                                                                                                                                                                                                                                                                            HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADR4), AND HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN INDONESIA/PIDW420). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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                                                                                                                 FUJIYAMA A., MIYANOHARA MATSUBARA K.;
                                                                                                                                          MEDLINE;
                                                                                                                                                       STRAIN-ADR4
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           STRAIN-ADR;
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                                        STRAIN-ADW;
                                                    SEQUENCE FROM
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176; Conser
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170
183 AA;
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larity 96.2%;
Conservative
                                                                                                    structural analyses of hepatitis
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
              SAKUGAWA
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Pred. No. 1.:
4; Mismatcl
                                                                                                                            NOZAKI C., YONEYAMA T., OHTOMO
              H., SASTROSOEWIGNJO R.I.,
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..24e-221;
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01-AUG-1990
01-FEB-1991
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EMBL; X01587; G59407; -.
EMBL; D00331; -; NOT_ANNOTATED_CDS.
PIR; A93480; NKVLA5.
PIR; B93460; NKVLA4.
PIR; C28925; NKVLJ3.
EMBL; D00329; PIR; A28925; N
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                                                                                                                                                   MEDILINE: 89010694.

OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO R OKAKAWA Y., MAYUMI M.;

"Typing hepatitis B virus by homology in nucleotide comparison of surface antigen subtypes.";

J. GEN. VIROL. 69:2575-2583(1988).
                                                                                                                                                                                                                                                                                CORE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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J. GEN. VIROL. 69:2575-2583(1988).
                                                                                                                                                                                                                                                                 HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN JAPAN/PJDW233)
VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNA
                                                                                                                                                                                                                                                                                                                                                                 CORA_HPBVJ
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CORE PROTEIN; REPEAT
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l similarity 95.6%;
175; Conservative
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(REL. 15,
(REL. 17,
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170
NKVLJ1
              -; NOT_ANNOTATED_CDS
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177
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 3.00e-221;
5; Mismatches 3;
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PFAM; PF00906; Hepat CORE PROTEIN; REPEAT REPEAT 162 1 REPEAT 170 1

Hepatitis_core;

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Matches 178; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONO Y., ONDA H., SASADA R., IGARASHI K., S "The complete nucleotide sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 83168919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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172
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96.2%;
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Pred. No. 5.93e-219;
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Pred. No. 9.22e-219;
                                                                                                                                                                                                      4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 183;
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Best Local s
Matches 17
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BHAT R.A., ULRICH P.P., VYAS G.N.;
BHAT R.A., ULRICH P.P., VYAS G.N.;
"Molecular characterization of a new
a persistently infected homosexual ma
HEPATOLOGY 11:271-276(1990).
PIR: A37182; MYXLH3
PFAM; PF00906; Hepatitis_core; 1.
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P29178;
01-DEC-1992 (REL. 2
01-DEC-1992 (REL. 2
01-DEC-1992 (REL. 2
                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 93346970.
NAUMANN H., SCHAEFER S
GERLICH W.H.;
                                                                                                                                                                                                                                                        005495;
01-NOV-1995 (
01-NOV-1995 (
01-NOV-1995 (
CORE ANTIGEN.
  "Identification of a new hepatitis that expresses HBV surface antigen J. GEN. VIROL. 74:1627-1632(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORE
                                                                                                                                                                                          HEPATITIS B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE WAVIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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182
195 AA;
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llarity 93.5%;
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24, LAST SEQUENCE UPDATE)
24, LAST ANNOTATION UPDATE)
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22461 MW;
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ANNOTATION UPDAT
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a new variant of hepatitis B virus
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                                                                                                        .F.T.,
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adw4.
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Best Local :
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01-OCT-1989
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           VAUDIN M.,
HARRISON T.
                                                                                                                                                                                                                                                                                                                                                                                                 CORA_HPBVL
P12901;
                        EMBL; D00220; D1000603; -.
PIR; A28885; NKVLCP.
PFAM; PF00906; Hepatitis_core;
CORE PROTEIN; REPEAT.
REPEAT 162 169
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REPEAT
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                                                                                                                                                                                                    "The complete nucleotide sequence of the virus isolated from a naturally infected J. GEN. VIROL. 69:1383-1389(1988).
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CORE PROTEIN; REPEAT.
 SEQUENCE
                                                                                                                                                                                                                                                                     MEDLINE; 88258473.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          VIRUSES; RETROID
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171; Conser
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184
184
191
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212 AA;
183 AA;
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(REL.
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larity 92.9%;
Conservative
              170
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12, LAST SEQUENCE UI
14, LAST ANNOTATION
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203 3
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195 2
203 4 MW;
20999 MW;
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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Pred. No. 3.13e-217;
10; Mismatches 3;
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                                                                                                                                                                                                                                                       TSIQUAYE K.N.,
 1AFF57C9 CRC32;
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RESULT 15

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01-AUG-1992
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VALENZUELA P., QUIROGA M., ZALDIVAR J., GRAY P., (IN) FIELD B.N., JAENISCH R., FOX C.F. (EDS.); ANIMAL VIRUS GENETICS, PP.57-70, ACADEMIC PRESS, PIR; A94409; NKVLA3.
PFAM; PF00906; Hepatitis_core; 1.
CORE PROTEIN; REPEAT.
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P03148;
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VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 1.06e-215;
4; Mismatches 2;
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Pred. No. 2.83e-216;
6; Mismatches 4;
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SEQUENCE
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21-JUL-1986 (REL.
15-DEC-1998 (REL.
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                                                                                                                               SPECIES-WOODCHUCK HEPATITIS VIRUS
                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                   "ANDLART F., CHEN T.N., MANDART E.;
"Nucleotide sequence of a cloned woodchuck hepatitis comparison with the hepatitis B virus sequence.";
J. VIROL. 41:51-65(1982).
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SPECIES-WOODCHUCK HEPATITIS VIRUS
MEDLINE; 82216969.
                                                                                                                                                                                                                                                                                                                                                                                             WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS VIRUSES; RETROID VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORE ANTIGEN
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                              "Sequence comparison of woodchuck hepatitis
                                                       PURCELL R.H.;
                                                                                                      MEDLINE; 88101359
                                                                                                                                                                                                                                                                                                                                                                                          VIRUSES;
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RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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214 AA; ..24722 MW;
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01, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
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            ō,
       the genome.";
                                                                                  ROSENBLUM
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7 (WHY 7),
59 (WHY 59), AND
8 (INFECTIOUS CLONE) (WHY 8).
HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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Pred. No. 1.
5; Mismatc
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Best Local S
Matches 12
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P03153;
21-JUL-1986
21-JUL-1986
01-JAN-1990
                       "Nucleotide sequence of an infectious molecularly cloned ground squirrel hepatitis virus.";
J. VIROL. 51:367-375(1984).
                                                                                                                                  SEQUENCE;
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PIR; G32397; NKVLC4.

PIR; C32397; NKVLC4.

PIR; C32397; NKVLC3.

PFAM; PF00906; Hepatitis_core;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete nucleotide sequence of a molecular clone of woodchuck hepatitis virus that is infectious in the natural host."; PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
                                                                                                                                                                                                      GROUND SQUIRREL HEPATITIS VIRUS (GSHV).
VIRUŞES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 89184524.
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This SWISS-PROT entry is copyright.
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188 AA;
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LAST
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ANNOTATION UPDAT
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Pred. No. 5.93e-146;
25; Mismatches 32;
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Query Match 50.3%;
Best Local Similarity 66.3%;
Matches 124; Conservative
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                                                                                                               REPEAT
SEQUENCE
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MEDLINE: 86062931.

KODAMA K., OGASAWARA N., YOSHIKAWA H., MURAKAMI S.;.

"Nucleotide sequence of a cloned woodchuck hepatitis virus

evolutional relationship between hepadnaviruses.";

J. VIROL. 56:978-986(1985).
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                      EMBL; M11082; G336135; -.
PIR; A03714; NKVLC2.
PFAM; PF00906; Hepatitis_core;
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01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
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PIR; A03715; NKVLS.
PFAM; PF00906; Hepatitis_core; 1.
CORE PROTEIN; REPEAT.
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21579 MW; A1C354F3 CRC32;
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Score 933; DB 1; Le
Pred. No. 5.20e-145;
26; Mismatches 33;
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Dec 16 13:02:42 1999; MasPar time 18.20 Seconds 743.783 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US3835-1-38183 (1-248) from us3835-1-38183.pep 1854 1 MDIDDYKEFGATVELLSFLP......RRRRSQSPRRBRSQSRESQC 248

Scoring table: PAM 150 Gap 11

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.830; Variance 106.555; scale 0.439

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1374 1374 1377 1377 1377 1377 1366 1366 1366 1366	Score
74.1. 74.1. 74.1. 73.9.9. 73.8.8.9.7. 73.7.8.8.9.7. 73.5.5.7.7.3.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9	Query Match
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72.3 72.3	72.3	72.3	72.4	72.4	72.5	72.5	72.5	72.7	72.7	72.7	72.8	72.9	72.9	72.9	73.1	73.2	73.2	73.3	73.4	73.4	•	73.5	•
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5.26e-215 5.26e-215		5.26e-215	.44e-	2.25e-215	1.47e-2	1.47e-215	9.62e-21		. 69e-		1.76e-216			4.91e-217	1.37e-217	5.86e-218	. 86e-		۲,	1.64e-218	1.64e-21		4.5/e-21

SO	DR R	אָט	DR	DR	DR	DR	DR	DR	DR	RL	RA	RA ?	0 :	R :	7	7 ; -	짇	RA	RX X	RP	RN	RĽ	RA	<del>2</del>	ŖР	RN	R.	RA	R C	ŖΡ	R	8	လ္လ	G N	DE	DT.	ဌ	ΡŢ	A	RESULT	
SEQUENCE 212 AA; 24350 MW; 71EA2C82 CRC32;	PFAM; PF00906; Repatitis_core; 1.	X85312; G736193;				x85283;	EMBL; X85313; G736196;		x85290; G736116;	1. 279:386-39	GREN E.Y., TSIBINOGIN V.V., KUKAIN R.A.;	BORISOVA G.P., PUMPEN P.P., BYCHKO V.V., PUSHKO P.M., KALIS Y.V.,	T NO N		NATION 1: 1: (CFF: )	cold ".	ide sequence of the henatities & virus genome (subtype	F., MANDART E., FITOUSSI F.,	1018	SEQUENCE FROM N.A.		ଟ-1	PLUCIENNICZAK A.;	YW4;	SEQUENCE FROM N.A.	[2]	(MAR-1995) TO EMBL/GENBANK/DDBJ DATA I		ATIEN	SEQUENCE FROM N.A.		RET		PRE-C/CORE.	PRE-C/CORE.	08, LAST ANNOTATIO	(TREMBLREL. 01,	(TREMBLREL.		LT 1 089656 PRELIMINARY: PRT: 212 AA.	

Match

Length

212;

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RESULT 2
1D 089437;
AC 089437;
DT 01-NOV-1
DT 01-NOV-1
DT 01-NOV-1
DE X, PREC
GN CORE.
OS HEPATITI
OC VIRUSES;
RN [1]
RP SEQUENCE
RC STRAIN-F
RA LAI M.E.
RL SUBMITTE
RN [2]
RP SEQUENCE
RC STRAIN-F
RA KARAYIAA
RL SUBMITTE
RN [3]
RP SEQUENCI
RC STRAIN-F
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RL SUBMITTE
RN [3]
RP SEQUENCI
RC STRAIN-F
RA KARAYIAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
X, PREC AND C GENES (CASTAA 2).
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E
                                                                                                                                                                                                                                                                                                                       KARAYIANNIS P.;
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182; Conservative
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Pred. No. 6.51e-221;
1; Mismatches 0;
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0C504D47 CRC32;
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. No. 2.78e-221;
Mismatches 0;
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Q68020;
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Q68008;
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X, PREC AND
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LIAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85284; G736098; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 183 AA; 21102 MW; BBE9AFBB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                           LAI M.E., MAZZOLENI A.P., PORRU A., BALES: SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ EMBL; X85291; G736119; -.
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HEPATITIS B VIRUS.
HEPATITIS PETROID VIRUSES;
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VIRUSES; RETROID VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00906; Hepatitis_core; SEQUENCE 212 AA; 24336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-PATIENT CASTAG-1'85;
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                          VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSP 208
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  VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
                                                                                          LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
                                                                                                               LCWGDLMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLIFGRETVIEYL 148
                                                                                                                                                                                  SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRE
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l similarity 99.5%;
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C GENES (FERRACUTI 1).
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llarity 98.98;
Conservative
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Pred. No. 6.51e-221;
1; Mismatches 0;
                                                                                                                                                                                                                                                                     Score 1374; DB 14;
Pred. No. 4.26e-221;
2; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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E0E4C243
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K/DDBJ DATA BANKS
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Best Local
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SUBMITTED (SEP-1995) TO EMBL/GENE
EMBL; X72702; G288930; -.
EMBL; X80925; E198084; -.
EMBL; X80925; E198084; -.
EMBL; X80906; Hepatitis_core; 1
PPAM; PP00906; Hepatitis_core; 1
AB; 24336 MW; 5
                                                                                                                                                                                                                                                                 Matches
                                                            Q67876;
Q67876;
Q1-NOV-1996
Q1-NOV-1996
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Q89597
Q8°
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01-NOV-1996
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MEDLINE; 94079539.
PREISLER-ADAMS S., SCHLAYER M.J.,
SEQUENCE FROM N.A.
STRAIN-PATIENT CI, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A.,
                                            PRE C/C ORF.
HEPATITIS B VIRUS.
                                     VIRUSES;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          RASENACK J.;
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G (TREMBLREL.
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(TREMBLREL.)
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                                   VIRUSES;
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                                   HEPADNAVIRIDAE;
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                                                           , CREATED)
, LAST SEQUENCE UP
, LAST ANNOTATION
                                                                                                                                                                                                                                                             Score 1374; DB 14;
Pred. No. 4.26e-221;
2; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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575D20BF CRC32;
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                                   ORTHOHEPADNAVIRUS
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                                                            UPDATE)
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AC Q6
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Best Local S
Matches 18
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Best Local 9
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RAO B.S., CASEY J.L., RINAUDO J.S.

RAO B.S., CASEY J.L., RINAUDO J.S.

SUBMITTED (MAR-1997) TO EMBL/GENI

EMBL; U95551; G2182120; -...

PFAM; PF00906; Hepatitis_core; 1

SEQUENCE 212 AA; 24360 MW; 7
                     JLT 8
Q68066;
Q68066;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
X, PREC AND
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EMBL; X65258; G59436; T.
PFAM; PF00906; Hepatitis_core;
PFAM; PF00906; Hepatitis_core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oll884 PRELIMINARY; PRT; 212 AA.
Oll884;
Ol-JUL-1997 (TREMBLREL. 04, CREATED)
Ol-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
Ol-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CORE ANTIGEN PRECURSOR.
HEPATITIS B VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRUSES; RETROID VIRUSES;
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                                                                                                                                                                                                                   VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
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                                                                                                                                                                                                                                                                                                              182;
                                                                                                                                                                                                                                                                                                                         Similarity
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                    (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
C GENES (LICHERI 2).
                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                            Conservative
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98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                                                                                                                                                                                                                            Score 1372; DB 14;
Pred. No. 9.96e-221;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1373; DB 14;
Pred. No. 6.51e-221;
2; Mismatches 0;
                                                                                PRT;
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6ED741BE CRC32;
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HEPATITIS B VIRUS

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Best Local Similarity
Matches 182; Conser
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268025
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Q68068;
Q1-NOV-1996
Q1-NOV-1996
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STRAIN-PATIENT LICHERI-3'90;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85315; G736207; -.
EMBL; X85315; G736207; -.
SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;
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STRAIN-PATIENT LICHERI-2'87;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85314; G736504; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 183 AA; 21102 MW; 6F38AA3B CRC32;
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Pred. No. 2.33e-220;
1; Mismatches 1;
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Best Local S
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01-NOV-1996
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PRE-C/CORE.
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Q67872;
Q1-NOV-1996
Q1-NOV-1998
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LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., I
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X65257; G59431; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24348 MW; A6BD9DA1 CRC32;
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HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
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SUBMLTITED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X85293; G736126; -.
PFAM; PF00906; Hepatitis core; 1.
SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;
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STRAIN=PATIENT CASTAG'3;
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    ESQC
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                                                                                       VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
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ilarity 98.4%;
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Pred. No. 3.57e-220;
2; Mismatches 1;
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STRAIL=PATIENT VITTORINA'92;

LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI

SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E

EMBL; X85256; G736052; -.

PPAM: PF00906; Hepatitis_core; 1.

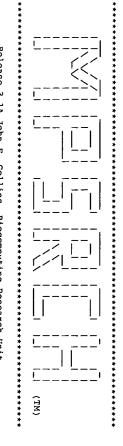
SEQUENCE 212 AA; 24322 MW; 83D9780B CRC32;
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Q67984;
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LIAM M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E EMBL; X85296; G736139; -
PFAM; PF00906; Hepatitis core; 1.
SEQUENCE 212 AA; 24308 MW; 69D87B53 CRC32;
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VIRUSES; RETROID V
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VIRUSES; RETROID VIRUSES;
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                                                                                                       SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 124
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181; Conser
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                                                                                                                                                                                                                                      Score 1369; DB 14;
Pred. No. 3.57e-220;
3; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3.57e-220;
1; Mismatches 1;
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PRE-C/CORE.
PRE-C/CORE.
HEPATITIS B VIRUS.
HEPATITIS B VIRUS.
                                                                          STRAIN-PATIENT GIORDO'84;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X853164 G736210;
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212, AA; 24376 MM; 80F52D0F CRC32;
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LAIM.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMINITED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85285; G756100; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24292 MW; 04A4D12D CRC32;
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HEPATITIS B VIRUS.
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181; Conservative
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182; Conser
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larity 98.9%;
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Pred. No. 5.
2; Mismatc
  Score 1366; DB 14;
Pred. No. 1.28e-219;
1; Mismatches 1;
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Sear Job	Qy	Db	Qy	Дb	Qy	Db	Qy	DЬ
ch con	245	209	185	149	125	8 9	65	29
Search completed: Thu Dec 16 13:04:25 1999 Job time : 103 secs.	245 ESQC 248	ESQC 212	185 VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 244	149 VSFGVWIRTPPAYRPPNAPILLTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 208	125 LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 184	LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 148	65 SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 124	29 GMDIDDYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 88

US3835-10-38183
MDIDPYKEFGATVELLSELPSDFFPSVRDLLDTASLLLQMDFGFPEHLLVDFLQSLSMDIDPYKEFGATV
ELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCMGELMTLATWYGVNLEDPASRD
LVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLVSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRG
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Dec 16 13:08:54 1999; MasPar time 11.54 Seconds 442.105 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US3835-10-38183 (1-240) from us3835-10-38183.pep 1796 1 MDIDPYKEFGATVELLSFLP.....RRRRSQSPRRRRSQSRESQC 240

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 33.355; Variance 174.564; scale 0.191

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Length	DB.	ĬĎ	Description	Pred. No.
1	1375	76.6	194	32	W50242	Hepatitis B virus pre	6.00e-99
2	1375	76.6		3	W50250	B virus	6.00e-99
ω	1375	76.6		u	R27473	protein.	6.00e-99
4	1363	75.9	184	μ.	P80959	Hepatitis B virus sub	5.67e-98
ភ	1359	75.7		3	W50241	Hepatitis B virus pre	1.20e-97
o	1358	75.6		32	W50251	Hepatitis B virus p21	1.44e-97
7	1353	75.3		20	W09044		3.68e-97
89	1349	75.1		-	R05635	Hepatitis B antigen.	7.78e-97
9	1349	75.1		Ç	P00041	Sequence of core anti	7.78e-97
10	1344	74.8		20	W09048	Plasmid pHBV DN AA en	1.98e-96
11	1338	74.5		v	P00004	Sequence of core anti	6.09e-96
12	1336	74.4		8	R40806	Hepatitis B core / PV	
13	1337	74.4		œ	R40808	Hepatitis B core / PV	7.35e-96
14	1334	74.3		4	P40311	Hepatitis virus core	1.29e-95
15	1334	74.3		œ	R40805	Hepatitis B core prot	1.29e-95
16	1334	74.3		13	R68868	w	1.29e-95

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ced sequence of f 8.36e-9 ve HBCAg protein. 8.36e-9 ve HBCAg protein. 8.36e-9 antigen of HBV. 1.47e-9 titis B virus pol 1.77e-9	85 6 R30781	ω	3	29
ced sequence of f 8.36e-9 ve HBcAg protein. 8.36e-9 ve HBcAg protein. 8.36e-9 antigen of HBV. 1.47e-9	83 13 R68869	ω	32	28
ced sequence of f 8.36e-9 ve HBcAg protein. 8.36e-9 ve HBcAg protein. 8.36e-9	85 26 P30061	ω	32	27
ced sequence of f 8.36e-9	85 6 R31025	ω.	32	26
duced sequence of f 8.36e-9	85 6 R30780	ω.	32	25
	85 10 R55284	ω.	32	24
patitis B core anti 8.36e-9	85 6 R30861	ω.	32	23
asmid phBV DN BB en 6.94e-9	89 20 W09049	ω.	32	22
duced amino acid se 6.94e-9	14 1 P90702	ω	32	21
patitis B virus pol 6.94e-9	83 13 R68866	ω	32	20
eS1 full length cor 3.96e-9	93 10 R55286	ω	32	19
patitis B core / IL 1.55e-9	98 8 R40807	٠.	ü	18
is B Virus cor 1.29e-9	83 12 R62869	٠.	33	17

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                                                                                                                                                                PT DNA encoding proteins which can be incorporated with wild type principles of viral replication, especially hepatitis B virus Prinhibition of viral replication, especially hepatitis B virus Ps Claim 15; Page 35; 60pp; English.

CC protein that is encoded by the full-length HBV precore gene. CC protein that is encoded by the full-length HBV precore gene. CC protein that is encoded by the full-length HBV precore gene. CC protein can be incorporated into HBV nucleocapsids along CC with the p21 core protein (see W50251), which is the usual nucleocapsid component, and thereby render the nucleocapsid component and thereby render the p22 (see W50242), p18 (see W50236). Met-p18 (see W50237) and Met-p28 (see W50242), p18 (see W50236). The inhibitory proteins can be produced by recombinant methods using claimed expression vectors and host cells. They can be provided exogenously to the target cells for use in inhibiting HBV replication. Alternatively, a nucleic acid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.
                                                                                   Query Match
Best Local Similarity
Matches 183; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Viral replication; inhibitor; HBV; nucleocapsid; gene therapy; hepatocyte; liver; p25 protein.

Hepatitis B virus.

W09809649-A1.
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Sequence 194 AA;
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03-SEP-1996; US-025370.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, Wands
MPI; 98-193325/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                   esqc 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lcwgelmtlatwogvnledpasrdlvvsyvntnmglkfrqllwfhiscltfgretvieyl 130
              SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
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                                                                                           76.6%;
larity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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99.5%;
                                                                                                              .56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 AA
                                                                                         Score 1375; DB 32;
Pred. No. 6.00e-99;
1; Mismatches 0;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1375; DB 32;
No. 6.00e-99;
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                                                                                           Gaps
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RESULT RE
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                                                                                                                                                                DR N-ESDB; (29105.)

Pr Vaccine comprises recombinant, attenuated pox-virus - use for pr vaccinating against viral infections such as rabies, hepatitis B, PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

CC Comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/CC core) which is precisely linked to the I3L promoter derived from CC vaccinia virus. This DNA sequence was linked to the S1 and S2 core) which is precisely linked to the I3L promoter derived from CC vaccinia virus. This DNA sequence was linked to the S1 and S2 core combinant expressing the HBV gene. Other HBV genes were also used to the construction of a NYVAC recombinant expressing the HBV gene. Other HBV genes were also used to the construction. These were HBV M protein (small pre-S antigen, cospady) and HBV L (large pre-S antigen, lpsAg). Each of these gene companies were inserted individually into three different sites of CC vaccinia virus which has been modified by deletion of six non-essential regions of the genome encoding known or potential virulence factors. The deletion loci were engineered as recipient loci for the insertion of the that any recombination that did occur would lead to disruption of the CC cascol-sea
     Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09215672-A.
17-SEP-1992.
09-MAR-1992; U01906.
07-MAR-1991; US-66056.
11-JUN-1991; US-713967.
06-MAR-1992; US-847951.
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R27473;
R27473;
R27473;
S12/core protein.
Hepatitis B virus; HBV; M protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (VIRO-) VIROGENETICS CORP.

COX WI, De Taisne C, Francis J, Gettig RR, Johnson GP,
Limbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus S
Riviere M, Tartaglia J, Taylor J;

WPI; 92-331718/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg vaccinia virus; 13L; promoter; NYVAC; recombinant; HBV L; large pre-S antigen; lpsAg; fusion protein; pre-S region; Sl2 S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                    Q35501-864
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     l Similarity
183; Conser
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                                                                                                                      346
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109..163
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164..346
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99
                                . 58
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                                   Score 1375;
Pred. No. 6.
DB 5; L-
6.00e-99;
                                                              Length
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В

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Conservative

1;

Mismatches

Indels

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Gaps

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TRESULT
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RESULT
ID WI
AC WI
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PR 07-OCT-1987; US-939617.

PR 07-OCT-1987; US-93617.

PR 07-OCT-1987; US-939617.

PR 07-
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Best Local S
Matches 18
T 5
W50241 standard;
W50241;
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Conjugate; fusion protein; hepatitis B core protein; HBV subtype ayw.;
T cell stimulating polypeptide; vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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P80959;
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183; Conse
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larity 99.5%;
Conservative
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                            Protein;
                                   193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1363; DB Pred. No. 5.67e-0; Mismatches.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PT DNA encoding proteins which can be incorporated with wild type
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT inhibition of viral replication, especially hepatitis B virus
PS Claim 9; Page 34-35; 60pp; English.

CC crotein that is produced by elimination of the 19-amino acid leader
CC protein that is produced by elimination of the 19-amino acid leader
CC protein that 25 kDa full-length HBV precore protein (see
CC the presence of high levels of HBV precore protein is inhibited in
CC the presence of high levels of HBV precore protein is inhibited in
CC the presence of high levels of HBV precore or precore-related
CC proteins. These proteins can be incorporated into HBV nucleocapsids
CC along with the p21 core protein (see w50251), which is the usual
CC nucleocapsid component, and thereby render the nucleocapsids
CC expression of the precore proteins, or certain variants of them,
CC leads to transdominant inhibition of HBV replication. Suitable
CC inhibitory proteins include p25 (see w50250), p22, Mat-p22 (see
CC w50242), p18 (see w50236), Met-p18 (see w50237) and Met-p18-Het
CC (see w50238). HeteroLogous peptides (see w50237) and Met-p18-Het
CC (see w50238). HeteroLogous peptides. The inhibitory
CC proteins can be produced by recombinant methods using claimed
CC expression vectors and host cells. They can be provided exogenously
CC to the target cells for use in inhibiting HBV replication.
CC alternatively, a nucleic acid construct that directs overexpression
CC therapy of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 181; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1998 (first entry)
Hepatitis B virus precore p22 polypeptide.
Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
hepatocyte; liver; p22 protein.
Hepatitis B virus.
                               Hepatitis B virus p21 core protein.

Viral replication; inhibitor; HBV; nucleocapsid;
hepatocyte; liver; p21; core protein.
Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP
Melegari M, Scaglioni PP,
WPI; 98-193325/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Region
                                                                                                    W50251;
28-SEP-1998 (first entry)
                                                                                                                                     W50251 standard; Protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy of
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                                                                                                                                                                                                        ESQC 240
                                                                                                                                                                                                                                                                                                                                           esqc 193
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                                                                                                                                                                                                                                                                            VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
                                                                                                                                                                                                                                                                                              vsfgvwirtppayrppnapilstlpettvvrrrgrsprrrtpsprrrrsgsprrrrsgsr 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.7%;
llarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection.
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 Location/Qualifiers 72..88
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TAL CORP.
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Pred. No. 1.20e-97;
2; Mismatches 1;
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                                                                  gene
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Best Local
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12 MAR-1998.
13 - SEP-1997; U15500.
03 - SEP-1996; US-025370.
(GEHO) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, Wellegari M, Scaglioni PP, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and thereby render the nucleocapsids deficient in encapsidating HBV pregenomic RNA. Thus, over-expression of the precore proteins or certain variants of them, leads to transdominant inhibition of HBV replication. Suitable inhibitory proteins include p25 (see W50250), p22 (see W50241), Met-p22 (see W50242), p18 (see W50235), Met-p18 (see W50237) and Met-p18-Het (see W50238). These proteins can be produced by recombinant methods using claimed expression vectors and host cells, and can be provided exogenously to target cells for use in inhibiting HBV replication. Alternatively, a nucleic acid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding proteins which can be incorporated with wild type nucleocapsid subunit(s) into a viral nucleocapsid useful for inhibition of viral replication, especially hepatitis B virus Disclosure; Page 41-42; 60pp; English.

This is the 21 kDa (p21) protein of hepatitis B virus (HBV) the assembled into a 180 kSa subunit nucleocapsid structure that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus core protein.
Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus; ground squirrel hepatitis B virus; duck hepatitis B virus;
                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promotes viral replication. Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsids along with the p21 core protein
                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core
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                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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181; Conse
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ilarity 98.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replication;
                                                                                                                                                                                                     /note= "C-terminus of core protein is at acid position between 71-180 in mutant polypeptides of the invention (Claim 23)" 81..180
                                                     acid position between polypeptides of the in 171..180
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 71..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                   /note= "C-terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "immunodominant region"
                  "C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1358; DB 32;
Pred. No. 1.44e-97;
1; Mismatches 1
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                                                                                              the invention
                      Of.
                                                                                                                             core protein
81 and 180 in
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                      core
                  protein
                                                                                          .80 in mutant (Claim 5)"
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Hépatitis B a
Hepatitis B v
Synthetic.
EP-374869-A.
27-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 55-56; 83pp; English.

Alteration of the C-terminus of the core protein (W09044) of hepatitis B virus (HBV) or other hepadnavirus creates a mutant polypeptide capable of reducing replication of the wild-type virus by a dominant negative mechanism. The inhibitory effect is species-specific and is achieved by deletion of a few C-terminal amino acids from the core protein, and/or by joining the core protein to a hepadnavirus surface protein (see also W09045), creating a core-surface fusion. Such mutant polypeptides (see also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9700698-A1.
09-JAN-1997.
20-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New method for inhibiting the replication of hepadnaviruses -
comprises introducing a mutant polypeptide with a mutated core
protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-1995; US-017814.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
WPI; 97-087176/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference
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                                                           R05635;
30-OCT-1990
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                                                                                    R05635
                                                                                                                                                                                                                                                                                                                                                                                  .nfection.
                                                                                                                                 238
                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                             sfgvwirtppayrppnapilstlpettvvrrpgrsprrrtpsprrrrsgsprrrrsgsre
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                                                                                                                                                                                                                                                                                                                       ch 75.3%;
l Similarity 98.9%;
181; Conservative
                                                                                   standard; protein; 183
                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                       183
                                    antigen.
virus; vaccine;
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                                                          (first entry)
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174..180
/note= "C-ter
                                                                                                                                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
172..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminus of core position 178 in mutant poly invention (Claim 7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminus of c
position 178 in mutant
invention (Claim 7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "amino acid residues 172-183,
are deleted from the core protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 in m
                                                                                                                                                                                                                                                                                                                       Score 1353; DB Pred. No. 3.68e-0; Mismatches
                                     HBV;
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(Claim
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Query Match
Best Local S
Matches 17
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22-DEC-1978; GB-049907.

27-DEC-1978; GB-050039.

01-NOV-1979; GB-037910.

(BIOJ) Biogen Inc.

Murray K, Schaller HE;

WPI: 90-195067/26.

N-PSDB; Q04799
                                                                                                                                                                                                                                                                                  06-AUG-1980.
21-DEC-1979; 303017.
22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
                                                              Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Example; Figs 3-4; 43pp; English. Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contg, pellet which was labelled with 3H or 32P as described by P. Ont, Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-PSt I dG:
                                                                                                                                                                                                                                                                                                                                                     14-OCT-1992 (first entry)
Sequence of core antigen.
Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
Hepatitis B virus.
EP--13828-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA encoding Hepatitis B virus polypeptide antigens used in detection of infection and in vaccine prodn. Disclosure; 4pp; English.

Polypeptide fragments encoded by the DNA sequence are antigenic for HBV and may be used as a vaccine or in detection. Peptides may be cultured in a suitable bacterial host such as E.coli.

Fragments of the sequence are also claimed as being antigenically
                                                                                                                                                                                                                               (BIOJ ) BIOGEN NV.
Murray K, Schaller HE;
WPI; 80-57268C/33.
N-PSDB; N00003.
                                                                                                                                                                                                                                                                                                                                                                                                                            P00041;
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177; Conser
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75.1%;
ilarity 96.7%;
Conservative
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ilarity 96.7%;
Conservative
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            1349; DB 5;
No. 7.78e-97;
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No. 7.78e-97;
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Best Local :
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09-JAN-1997.
20-JUN-1995; U10602.
20-JUN-1995; US-017814.
(GEHO) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
WPI; 97-087176/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09048 stand
W09048;
11-APR-1997
Plasmid pHBV
                                                                                                                                                                Plasmid phby DN AA carries an insert (T49598) coding for a protein (W09048) comprising a hepatitis B virus (HBV) core protein (see also W09044) fused in-frame at amino acid 179 with the HBV surface protein (see also W09045) at amino acid 8. Plasmid phBV DN BB (T49599) expresses the HBV core fused at amino acid 175 to the surface protein at amino acid 112 (W09049). phBV DN AA was at least as potent an inhibitor of HBV replication as construct pHBV DN (T49597); phBV DN BB was less inhibitory than phBV DN. Vectors expressing hepadnavirus dominant negative core mutants can be utilised in the gene therapy of viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1997 (first entry)
Plasmid pHBV DN AA encoded HBV dominant negative polypeptide.
Hepadnavirus; woodchuck hepatitis virus; hepatitis delta viru
HBV; ground squirrel hepatitis B virus; duck hepatitis B viru
core protein; replication; antiviral; gene therapy; pHBV DN A
                                                                                                                                                                                                                                                                                                                            N-PSDB: T49598.

N-PSDB: T49598.

New method for inhibiting the replication of hepadnaviruses comprises introducing a mutant polypeptide with a mutated core protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
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Key
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                                                                                                                   74.88;
1 Similarity 100.08;
179; Conservative
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/note= "positions 1-179
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9-226 of HBV surface protein"
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                                                                                                                   Score 1344; DB Pred. No. 1.98e 0; Mismatches
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Best Local S
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06-AUG-1980.
21-DEC-1979; 303017.
22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
                                                                                                                                                                                                                                                                         Hepatitis
Hepatitis
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Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contry pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dG: HBV-Kpn I dC: Tetk AmpS HBV+.
       J05192170-A.
03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NIST ) NISSHIN OIL MILLS LTD.
                                                                                                                                                                                                                                Synthetic.
Key
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R40806 standard; Protein; 196
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Murray K, Schaller HE;
WPI; 80-57268C/33.
N-PSDB; N00002.
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l Similarity 96.2%;
177; Conservative
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14..196
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Pred. No. 6.09e-96;
5; Mismatches 1
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Best Local Similarity
Matches 175; Conser
                                                                                                                                                                                                                                                                                                                                                               03-AUG-1993; 243800.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW) NISSHIN OIL MILLS L
WPI; 93-277479/35.
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Hepatitis
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R40808 standa
R40808;
16-FEB-1994
                                                                                                                                                                                                    Recombinant plasmid for high immunogenity virus - or recombined haemagglutinin gene, hepatitis B core gen virus and exotic genes
Disclosure; Fig 9; 12pp; Japanese.
The hepatitis B core gene is recombined with PV-1 DN and IL-1 beta to form a plasmid (Q47738) which is the a vaccine. NB: Sequence is difficult to read in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant plasmid for high immunogenity virus - contains recombined haemagglutinin gene, hepatitis B core gene of vaccinia virus and exotic genes Disclosure; Fig 7; 12pp; Japanese.

The hepatitis B core gene is recombined with PV-1 DNA and IL-1 beta to form a plasmid (047738) which is then used to properly the property of the prop
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N-PSDB; Q47736.
                                                                                                                                                                Seguence
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                                                                               ch 74.4%;
l Similarity 94.6%;
175; Conservative
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larity 95.18;
Conservative
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26..208
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PV-1; IL-1 beta;
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                                                                               Score 1337;
Pred. No. 7.
7; Mismatcl
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Pred.
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                                                                               re 1337; DB 8; L
d. No. 7.35e-96;
Mismatches 3;
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d. No. 8.86e-96;
Mismatches 3;
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the original
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19-OCT-1982; 183432.

18 19-OCT-1982; JP-183432.

19 -OCT-1982; JP-183432.

19 -OCT-1982; JP-183432.

10 -OCT-1982; JP-183432.

11 19-OCT-1982; JP-183432.

12 19-OCT-1982; JP-183432.

13 18 WPI; 84-143231/23.

15 DNA used in prevention of infections by hepatitis virus B - coding gene and at least 1 virus core antigen structural gene.

15 Disclosure; Fig 3; 13pp; Japanese.

16 Disclosure; Fig 3; 13pp; Japanese.

17 The sequence is that of hepatitis virus core antigen (HBcAg). It can be used as a vaccine for the prevention of infections by hepatitis B virus (HBV) and also in the diagnosis of early stages of HBV infection. See also P40310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 17
                                                                                                                   03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS L
WPI; 93-277479/35.
N-PSDB; Q47735.
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HBCAg; vaccine; diagnosis; HBV
Hepatitis b virus.
Recombinant plasmid for high immunogenity virus - recombined haemagglutinin gene, hepatitis B core virus and exotic genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis b v
J59074985-A.
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16-FEB-1994
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R40805 standard; Protein; 183
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Local Similarity 95.6%;
Les 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       B core protein.
B; core; HBC; PV-1;
B Virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                               IL-1 beta; interleukin; plasmid
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                                                                                                                                                                                             Disclosure: Fig 6: 12pp: Japanese.
The hepatitis B core gene is recombined with PV-1 DNA
and IL-1 beta to form a plasmid (Q47738) which is then used to produce
a vaccine. NB: Sequence is difficult to read in the original
specification.
 238
                  181
                                     178
                                                       121
                                                                         118
                                                                                           61
                                                                                                            58
                                                                                                            sqc 183
                                   CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
                                                                                                                                                tch 74.3%; al Similarity 95.6%; 175; Conservative
                                                                                                                                                                                      183 AA;
                                                                                                                                                 Score 1334; DB 8; I
Pred. No. 1.29e-95;
5; Mismatches 3;
                                                                                                                                                                   Length 183;
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Search completed: Thu Dec 16 13:11:36 1999 Job time: 162 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:11:54 1999; MasPar time 12.41 Seconds 775.040 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US3835-10-38183 (1-240) from us3835-10-38183.pep 1796 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 240

Scoring table: PAM 150 Gap 11

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 47.190; Variance 119.785; scale 0.394

### SUMMARIES

222229876544322222222223322222222222222222222222	Result
1374 1374 1374 1373 1373 1370 1370 1369 1369 1369 1366 1366 1366 1366 1366	Score
776.5.2.2.2.3.4.4.5.5.6.5.2.2.2.3.3.4.4.5.5.6.5.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.6.5.2.2.2.2.2.3.3.3.4.4.5.5.5.2.2.2.2.2.3.3.3.4.4.5.5.5.2.2.2.2.3.3.3.4.4.5.5.5.2.2.2.2.2.3.3.3.4.4.5.5.5.2.2.2.2.2.3.3.3.4.4.5.5.5.2.2.2.2.2.3.3.3.4.4.5.5.2.2.2.2.2.3.3.3.4.4.5.2.2.2.2.2.2.3.3.3.4.4.5.2.2.2.2.2.2.3.3.3.4.4.5.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2	% Query Match
212 212 213 214 215 216 217 217 217 217 217 217 217 217 217 217	Length
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NKVLAH S32204 S53207 S53207 S53207 S53216 S53216 S53216 S53226 S53226 S53226 S53220 S53220	ID
e antigen precursor e antigen precursor e antigen precursor core antigen precursor e a	Description
6.47e-198 6.55e-198 6.55e-198 9.59e-198 9.59e-199 3.01e-197 4.40e-197 4.40e-197 4.40e-197 6.45e-196 2.96e-196 4.33e-196 4.33e-196 4.33e-196 4.33e-196 4.33e-196 4.33e-196 1.36e-195 1.36e-195 1.36e-195 1.36e-195	Pred. No.

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NKVLJ2	S53236	S25651	S53257	S53137	S53238	S53189	S53267	5314	S53229	S53214	S53152	5326	S53232	S53181	NKVLA2	S53240	S53129	S53242	NKVLBH	S53281	NKVLAI
			ecc		eg.	•	,	ഗ	601	•	•	•		•	മ	e antigen precursor /			e antigen precursor /		e antigen precursor /
.68e-19	5.93e-19	4.05e-192	2.77e-19	4.05e-19	9e-19	1.89e-192	9e-19	9e-1	6.03e-19	.83e-19	e	e-19	1.31e-19	8.98e-19	:_	4.19e-19	:_		9.13e-19	.26e-	.91e-

##molecule_type DNA ##residues 1-212 ##cross-references EM ##experimental_source ##accession \$53264 ##molecule_type DNA ##residues_type LNA ##residues_type DNA	##molecule_type DNA ##residues 1-2 ##cross-references ##experimental_sour #accession \$53209 ##molecule_type DNA ##residues 1-2 ##cross-references ##cross-references ##experimental_sour #accession \$53234	a such Such	REFERENCE #authors #submission #description #accession	DATE	RESULT 1 ENTRY TITLE ALTERNATE_NAMES CONTAINS ORGANISM #variety
##molecule_type DNA ##residues 1-212 ##label LA3 ##ressidues 1-212 ##label LA3 ##cross-references EMBL:X85300; NID:g736150; PID:g736152 ##experimental_source isolate patient Sanna'84 cession S53264 ##molecule_type DNA ##molecule_type DNA 1-212 ##label LA4 ##residues 1-212 ##label LA4 ##cross-references EMBL:X85313; NID:g736194; PID:g736196	##molecule_type_DNA ##rosidues 1-212 ##label LAI ##rosidues 1-212 ##label LAI ##cross_references_EMBL.x85283; NID:g736088; PID:g736090 ##experimental_source_isolate_patient_ferracuti'83 #ession S53209 ##molecule_type_DNA ##rosidues 1-212 ##label LA2 ##rosidues 1-212 ##label LA2 ##rosidues 1-212 #flabel LA2	##molecule_type DNA  ##residues 1-212 ##label PLU  ##cross-references EMBL:335716; NID:g527435; PID:g527437  ##cross-references subtype ayw4, isolate hb321  **RES  **S33112**  **CE  **S33112**  **CE  **Lhors  **Lhors  **Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  **Chassion  **S3101  **S	\$47404 Pluctenniczak, A. Pluctenniczak, A. Submitted to the EMBI Data Library, August 1994 Molecular cloning and sequencing of two complete genomes of polish isolates of human hepatitis B virus. \$47405	1801ate patient Licheri's 65; 1801ate patient riore's 66; 1801ate patient Licheri'83 18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change 10-Oct-1997 \$47405; \$53191; \$53209; \$53234; \$53264; \$53249; \$53262; \$55277; A03711	

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KEYWORDS
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ORGANISM
                                                                                                                      RESULT
ENTRY
TITLE
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Best Local S
Matches 18
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30-178
                 #variety
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#cross-references MUID:81012091
#accession A03711
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##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
##experimental_source isolate patient Licheri'83
##experimental_source isolate patient Licheri'83
                                                                                                                                                                                                                                                                                                                                              117
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##experimental_source patient Giordo-2'86
##note due to a stop codon between the alternative initiators
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cession S53262
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183; Conservative
                                                                                                                                                                                                         240
                                                                                                                    S53211
e anti
                                                                                    HBc antigen; HBe antigen
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isolate patient Castag-1'85; isolate patient Ferracuti-1'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                                                      core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence
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                                   #formal_name hepatitis B virus, HBV
                                                                                   antigen precursor / core antigen - hepatitis B
  (isolate patient Castag-1'85 and others)
BC antigen; HBe antigen precursor / HBc antigen;
                                                                    antigen
                                                   antigen; e antigen
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#product core antigen #status predicted #label CAG\
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#domain carboxyl terminal propeptide #link EAG #statu
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99.5%;
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1 212 #molecular-weight 24350
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Pred. No. 4.47e-198;
1; Mismatches 0;
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##cross-references EMBL:X72702; NID:g288927; PID:g288930
##experimental_source subtype ayw, patient C1000
##note due to a stop codon between the alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 30-212 ##label LAW
##cross-references EMBL:X85284; NID:9736095; PID:9736098
##note due to a stop codon between the alternative :
the e antigen precursor cannot be produced
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1-212 ##label LAI
##cross-references EMBL:x85291; NID:g736117; PID:g736119
                                                                     ##molecule_type DNA
##residues 1-212 ##label PRE
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Similarity 98.9%;
182; Conservative
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S53211; S53197
S53112
                                                                                                                                         Gerok, W.; Rasenack, J.
submitted to the EMBL Data Library, March 1993
Identification and sequence analysis of hepati
in immunological negative infection.
                                                                                                                                                                                                                                                                                                                                                                                                                    $32204 #type complete
e antigen precursor / core antigen -
(subtype ayw, patient C1000)
HBe antigen precursor / HBc antigen;
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                                                                                                                                                                                                                                                                                                                                subtype ayw, patient C1000
20-Feb-1995 #sequence_revision
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                                                                                                                                                                                                                                                                 S32202
                                                                                                                                                                                                                                                                                                                                                                             #formal_name hepatitis B virus,
                                                                                                                                                                                                                                                                                                                                                                                                   core antigen;
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
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Data Library,
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##cross-references EMBL:x85289; NID:g736110; PID:g736113
##experimental_source isolate patient Castaa-2'87
##note due to a stop codon between the alternative initiatiors
##note the e antigen precursor cannot be produced
 118
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l Similarity 98.9%;
182; Conservative
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Similarity 99.5%;
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#superfamily hepatitis B virus core antigen
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#length 183 #molecular-weight 21102 #chec
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S53112
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isolate patient Castaa-2'87
08-Jul-1995 #sequence_revision(
08-Sep-1997
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2; Mismatches 0;
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Pred. No. 9.59e-198;
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Sequence analysis of HBV genomes isolated
HBSAg negative chronic liver disease.
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  (subtype ayw, patient CI)
HBe antigen precursor / HBc antigen;
#formal_name hepatitis B virus,
isolate patient Licheri-2'87
08-Jul-1995 #sequence_revision ()
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Licheri-2'87)
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#formal_name hepatitis B virus,

subtype ayw, patient CI

20-Feb-1995 #sequence_revision:
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Pred. No. 9.59e-198;
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Matches 182;
                       Query Match 76.3%;
Best Local Similarity 98.9%;
                                                                                                              30-212
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##experimental_source isolate patient Licheri-2'87
##note due to a stop codon between the alternative initiatiors
the e antigen precursor cannot be produced
                                                                                                                                                                                                                                                                            ##cross-references EMBL:x85293; NID:g736124; PID:g736126
##experimental_source isolate patient Castag'3
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                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
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S53270
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S5311
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#formal_name hepatitis B virus, HBV
isolate patient Castag'3
08-Jul-1995 #sequence_revision 03-Aug-1995
08-Sep-1997
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HBe antigen precursor / HBc antigen;
core antigen; e antigen
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                                                                                                                                                                                                      alternative initiators; core protein
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#product e antigen #status predicted #label EAG\
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98.4%;
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       Score 1370; DB 2;
Pred. No. 3.01e-197;
1; Mismatches 1;
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Data Library, March 1995
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Data Library, March 1995
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Local Similarity 98.9%;
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S53163
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#formal_name hepatitis B virus, HBV
isolate patient Licheri-3'90
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
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HBe antigen precursor / HBc antigen;
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alternative initiators; core protein
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #statu
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 precursor / core antigen -
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Pred. No. 3.01e-197;

    Mismatches

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                           ##residues 1-212 ##label LAI
##cross-references EMBL:X65257; NID
##experimental_source subtype ayw,
                                                                  ##molecule_type DNA
##residues 1-2
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##experimental_source isolate patient Vittorina'92
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Similarity 98.9%;
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Sequence analysis of HBV genomes isolated from
HBSA9 negative chronic liver disease.
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e antigen precursor / core antigen -
(subtype ayw, patient C)
(subtype ayw, patient C)
HBe antigen precursor / HBC antigen;
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#formal_name hepatitis B virus,

subtype ayw, patient C

20_Feb-1995 #sequence_revision;
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#formal_name hepatitis B virus, HBV
isolate patient Vittorina'92
08-Jul-1995 #sequence_revision 03-Aug-1995
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#product core antigen #status predicted #label CAG\
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#domain carboxyl-terminal propeptide #link EAG #statu:
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                              NID:g59429; PID:g59431
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                                                                                                                   SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 116
                                                                                                                                          GMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 88
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to the EMBL Data Library, March 1995
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Pred. No. 4.40e-197;
2; Mismatches 1;
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3; Mismatches 0;
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##cross-references EMBL:X85285; NID:g736099; PID:g736100
##experimental_source isolate patient Ferracuti-2'90
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                                 core antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate pattent Chighine-1'85
08-Jul-1995 #sequence_revision 03-Aug-1995
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larity 98.4%;
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(isolate patient Chighine-1'85)
                      08-Sep-1997
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Pred. No. 6.45e-197;
2; Mismatches 1;
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Similarity 97.8%;
180; Conservative
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#formal_name hepatitis B virus, HBV
isolate patient Giordo'84
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                       S5327
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1 212 #molecular-weight 24364 #checksum 1123
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212 #molecular-weight 24376
76.1%;
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Pred. No. 1.38e-196;
3; Mismatches 1;
Score 1366;
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Data Library, March 1995
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##cross-references EMBL:X85275; NID:g736057; PID:g736060
##experimental_source isolate patient Muresu'89
##experimental_source isolate patient Muresu'89
##note due to a stop codon between the alternative initiations
the e antigen precursor cannot be produced
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                                                                                           181 SQC 183
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                                                               240
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Core antigen - hepatitis B virus (isolate patient Muresu'89)
HBC antigen
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MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Thu Dec 16 13:13:23 1999; MasPar time 8.61 Seconds 788.293 Million cell updates/sec

Tabular output not generated.

Title:
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>US3835-10-38183 (1-240) from us3835-10-38183.pep 1796 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 240

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 48.420; Variance 107.281; scale 0.451

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

22							15								7 1	6 1	5 1	4 1	3 1	2 1	1 1	Result	
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TONG S., LI J., VITVITSKI L., TREPO C.;
"Active hepatitis B virus replication in the associated with viral variants containing an
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OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO F
MIYAKAWA Y., MAYUMI M.;

"Typing hepatitis B virus by homology in nucleotide
comparison of surface antigen subtypes.";
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"Hepatitis B virus genes and their expression NATURE 282:575-579(1979).
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12,
                                                                                                                                                                                                           15, CREATED)
15, LAST SEQUENCE UPDATE)
17, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GILBERT W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21042 MW;
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LAST SEQUENCE UI
LAST ANNOTATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1349; DB 1;
Pred. No. 1.09e-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6EA6B674 CRC32;
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                                                                       SASTROSOEWIGNJO R.I.,
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RANGE REPORT OF THE SOLUTION O
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
SEQUENCE
  MEDLINE: 89010694.

OKAMOTO H., TSUDA F., S
MIYAKAWA Y., MAYUMI M.;
                                                                                                                                                                                             MEDLINE: 83246570.
FUJIYAMA A., MIYANOHARA
MATSUBARA K.;
"Cloning and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADR4), AND HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN INDONESIA/PIDW420). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. GEN. VIROL.
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              STRAIN-ADR4
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 ONO Y., ONDA H., SASADA R., IGARASHI K., S
"The complete nuclectide sequences of the
DNA; subtype adr and adw.";
NUCLEIC ACIDS RES. 11:1747-1757(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ADR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                             STRAIN-ADW
                                                                                                                                                  NUCLEIC ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 01, CREATED)
(REL. 01, LAST SEQUENCE UPDATE)
(REL. 17, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
170
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                                                                                                                                                  RES.
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21081 MW;
                                                                                                                                                  11:4601-4610(1983)
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                             SAKUGAWA
                                                                                                                                                                                                  analyses of hepatitis
                                                                                                                                                                                                                                            A., NOZAKI C., YONEYAMA T., OHTOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1336; DB 1;
Pred. No. 3.14e-219;
4; Mismatches 3;
                           н.,
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                             SASTROSOEWIGNJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183
                                                                                                                                                                                                                                                                                                                                                                                                                 SUGINO Y., NISHIOKA
e cloned hepatitis B
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                                                                                                                                                                                                    virus
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                             R.I.,
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                             IMAI
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Best Local :
                                                                        between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by inon-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement (See httpor send an email to license@isb-sib.ch).
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P17391;
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 89010694.
OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO R.I., IMAI MIYAKAWA Y., MAYUMI M.;
"Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes.";
J. GEN. VIROL. 69:2575-2583(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
CORE ANTIGEN.
HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN JAPAN/PJDW233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
SEQUENCE
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes.";
J. GEN. VIROL. 69:2575-2583(1988).
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
EMBL; D00329; -; NOT_ANNOTATED_CDS. PIR; A28925; NKVLJ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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D00331; NOT_ANNOTATED_CDS.

A93480; NKVLA5.

B93460; NKVLA4.

C28925; NKVLJ3.
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l Similarity 95.6%;
l75; Conservative
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170
183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REL. 15, CREATED)
(REL. 15, LAST SEQUENCE UI
(REL. 17, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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177
; 21095 MW;
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Pred. No. 7.
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Best Local S
Matches 17
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Best Local Similarity 96.2%;
Matches 176; Conservative
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21-JUL-1986
21-JUL-1986
01-OCT-1989
                                                                                                                                                                                                                                                                                                                          rram; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT. REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ONO Y., ONDA H., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONO Y., ONDA H., SASADA R., IGARASHI K., 9
"The complete nucleotide sequences of the
DNA; subtype adr and adw.";
NUCLEIC ACIDS RES. 11:1747-1757(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEPATITIS B VIRUS (SUBTYPE ADW).
VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORE ANTIGEN
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                           CWGELMTLATWVGNNLQDPASRDLVVNYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLV 120
                                                                                           MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
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  CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
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178; Conse
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170
183 AA;
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172
185 AA;
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(REL.
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01, LAST SEQUENCE UP
12, LAST ANNOTATION
                                                                                                                                                                                                                                                                                       21394 MW;
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                                                                                                                                                                                       Score 1321; DB Pred. No. 2.17e-4; Mismatches
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Pred. No. 1.40e-216;
3; Mismatches 4:
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                                                                                                                                                                                                                                                                                       791E0381 CRC32;
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ON UPDATE)
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2.17e-216;
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                                                                                                                                                                                                                                   Length 185;
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i hepatitis B
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Best Local Similarity 93.5%;
Matches 173; Conservative
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Q05495;

Q1-NOV-1995 (REL. :

01-NOV-1995 (REL. :

01-NOV-1995 (REL. :

CORE ANTIGEN.
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P29178;
01-DEC-1992 (REL.
01-DEC-1992 (REL.
01-DEC-1992 (REL.
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                        "Identification of a new hepatitis B virus that expresses HBV surface antigen subtype J. GEN. VIROL. 74:1627-1632(1993).
                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE: 93346970.
NAUMANN H., SCHAEFER S.,
GERLICH W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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"MOLECULAR Characterization of a new variant of hepatitis a persistently infected homosexual man.";
HEPATOLOGY 11:271-276(1990).
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RETROID V
                                                                                                                                                                                                                                                                                                       S B VIRUS (SUBTYPE RETROID VIRUSES; 1
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VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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32, LAST SEQUENCE SEQUENCE ANNOTATION OF THE PROPERTY OF THE PROP
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24, LAST SEQUENCE UP
24, LAST ANNOTATION
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22461 MW;
                                                                                                                                                                         YOSHIDA
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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Pred. No. 4.57e-215;
9; Mismatches 3;
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                                                                  (HBV) genotype adw4.";
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        "The complete nucleotide sequence of the virus isolated from a naturally infected J. GEN. VIROL. 69:1383-1389(1988).
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P12901;
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                                                                                                          EMBL; D00220; D1000603; -. PIR; A28885; NKVLCP.
                                                                                                                                                                                                                                                                                                                                                                                                             VAUDIN M., WOLSTENHOLME A.J., TSIQUAYE K.N., HARRISON T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEPATITIS B VIRUS
VIRUSES; RETROID '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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HEPADNAVIRIDAE; (
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      1AFF57C9 CRC32;
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Best Local S
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Best Local :
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P17099;
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01-AUG-1990 (
01-AUG-1992 (
CORE ANTIGEN:
C.
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01-AUG-1992
15-DEC-1998
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P03148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
SEQUENCE
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VIRUSES; R
                                                                                                            CORA_HPBV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VALENZUELA P., QUIROGA M., ZALDIVAR J., GF
(IN) FIELD B.N., JAENISCH R., FOX C.F. (EI
ANIMAL VIRUS GENETICS, PP.57-70, ACADEMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A94409; NKVLA3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                          RESQC 185
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                                                                                                                                                                                                                                                                                                                                      CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
                                                                                                                                                                                                                                                                                                                                                          CWGELMTLATWVGNULEDPASRDLVVNYVNTNVGLKIRQLLWFHISCLTFGRETVLEYLV 120
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177; Conser
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173; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B VIRUS (SUBTYPE ADW2).
RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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172
185 AA;
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ilarity 95.7%;
Conservative
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llarity 94.5%;
Conservative
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ANNOTATION UPDATE)
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ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1305; DB 1;
Pred. No. 2.30e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J., GRAY P., .F. (EDS.);
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. 6.23e-214;
                                                                                                              214
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Best Local :
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21-JUL-1986
15-DEC-1998
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VIRUSES; F
[1]
PURCELL R.H.; "Sequence comparison of woodchuck hepatitis shows conservation of the genome.";
                                                                                              SEQUENCE FROM N.A.
SPECIES-WOODCHUCK HEPATITIS VIRUS MEDLINE; 88101359.
                                                                                                                                                                                       GALIBERT F., CHEN T.N., MANDART E.;
"Nucleotide sequence of a cloned woodchuck hepatitis virus comparison with the hepatitiis B virus sequence.";
J. VIROL. 41:51-65(1982).
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. SPECIES-WOODCHUCK HEPATITIS VIRUS MEDLINE; 82216969.
                                                                                                                                                                                                                                                                                                                                                                                                    WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                 VIRUSES; RETROID VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P03152;
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                                                                          J.I., MILLER
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177; Conser
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RETROID V
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VIRUSES; HEPADNAVIRIDAE; OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01, CREATED)
01, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
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24722 MW;
                                                                          R.H.,
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                                                                          ROSENBLUM
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7 (WHV 7),
59 (WHV 59), AND
8 (INFECTIOUS CLONE) (WHV 8).
HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1304; DB 1;
Pred. No. 3.56e-213;
5; Mismatches 2;
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                                                                                                                        WOODCHUCK
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Matches 12
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EMBL; M18752; G336140; -.
EMBL; M19183; G336145; -.
EMBL; J04514; G336149; -.
PIR; A03713; NKVLC.
PIR; C32397; NKVLCT.
PIR; C32397; NKVLC4.
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MEDLINE; 89184524.

GIRONES R., COTE P.J., HORNBUCKLE W.E., TENNANT B.C., GERIN J.L., GIRONES R., COTE P.J., HORNBUCKLE W.E., TENNANT B.C., GERIN J.L., GIRONES R., COTE P.H., HORNBUCKLE W.E., TENNANT B.C., GERIN J.L., COMPLETE R.H.;

PURCELL R.H., MILLER R.H.;

"Complete nucleotide sequence of a molecular clone of woodchuck hepatitis virus that is infectious in the natural host.";

PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).

PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
                                                                                                                                                                                                                                                                                                                               P03153;
21-JUL-1986
21-JUL-1986
01-JAN-1990
                                            "Nucleotide sequence of an infectious ground squirrel hepatitis virus."; J. VIROL. 51:367-375(1984).
                                                                                                                                                                                                                                                                                                       CORE
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CORA_HPBGS
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SPECIES-WOODCHUCK HEPATITIS VIRUS 8
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                                                                                                                            SEEGER C., GANEM D.,
                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 84267998.
                                                                                                                                                                                                                            VIRUSES;
                                                                                                                                                                                                                                                         GROUND
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1 similarity 67.0%;
126; Conservative
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13, LAST ANN
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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ANNOTATION UPDATE)
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Pred. No. 2.07e-144;
25; Mismatches 32;
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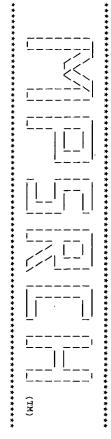
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Query Match 51.9%;
Best Local Similarity 66.3%;
Matches 124; Conservative
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P06433;
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CORE PROTEIN; REPEAT
196 203
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PIR; A03714; NKVLC2.
PFAM; PF00906; Hepatitis_core; 1.
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VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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l Similarity 68.1%;
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217 AA;
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211
25189 MW; B70A00B1 CRC32;
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Score 933; DB 1; Louis Pred. No. 1.77e-143; 26; Mismatches 33;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

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>US3835-10-38183 (1-240) from us3835-10-38183.pep 1796 1 MDIDPYKEFGATVELLSFLP.....RRRRSQSPRRRRSQSRESQC 240

Scoring table: PAM 150 Gap 11

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

179066 segs, 54579741 residues

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.641; Variance 107.390; scale 0.434

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

20 20 20 20 20 20 20 20	Result
1374 1374 1374 1373 1373 1373 1373 1370 1370 1369 1369 1369 1369 1369 1369 1366 1366	Score
77777777777777777777777777777777777777	% Query Match
211 212 213 214 215 217 217 217 217 217 217 217 217 217 217	Length
	DB
Q89556 Q689297 Q89437 Q89437 Q68908 Q67876 Q61884 Q68066 Q68066 Q68066 Q68068 Q68068 Q68069 Q68032 Q67872 Q68032 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030 Q68030	ĪD
PRE-C/CORE.  PRE-C/CORE.  HBCAG.  X, PREC AND C GENES (FRE C/C ORF.  CORE ANTIGEN PRECURSOR  X, PREC AND C GENES (L PRE-C/CORE. Y, PREC AND C GENES (M X, PREC AND C GENES (F PRE-C/CORE.) PRE-C/CORE.	Description
9.01e-219 1.37e-218 1.37e-218 2.09e-218 2.09e-218 2.09e-218 3.18e-218 7.37e-218 7.37e-218 7.37e-218 7.37e-217 1.12e-217	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
1341	1341	1341	1341	1342	1344	1344	1343	1345	1347	1348	1348	1349	1351	1351	1352	1355	1357	1357	1359	1360	1360	1360	1362	1363
74.7	74.7	74.7	74.7	74.7	74.8	74.8	74.8	74.9	75.0		75.1	75.1	٠	75.2		٠	٠	75.6		75.7	75.7		75.8	٠
212				183	212	212			212		183		212	183						212	212	212	212	212
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
Q81115	Q68042	Q68003	Q68064	067964	Q68035	092918	Q68023	Q67973	Q67912	068060	Q68037	Q67997	Q89719	Q67946	Q89531	Q68045	Q68077	Q68075	Q68053	Q96845	Q68016	Q89446	Q68051	Q67980
HBEAG, HBCAG.	PRE-C/CORE.	GENES (	X, PREC AND C GENES (L	C GENES (	PRE-C/CORE.	PRECORE PROTEIN PRECUR		X, PREC AND C GENES (T	PRE-CORE/CORE PROTEIN.	C GENES	X, PREC AND C GENES (D	D C GENES	PRE-C/CORE.	C ANTIGEN.	CORE PROTEIN.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	COMPLETE GENOME.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.
1.44e-212	1.44e-212	1.44e-212	1.44e-212	9.47e-213	4.09e-213	4.09e-213	6.22e-213	2.69e-213	1.16e-213	7.62e-214	7.62e-214	5.01e-214	2.16e-214	2.16e-214	1.42e-214	4.02e-215	1.74e-215	1.74e-215	7.50e-216	4.92e-216	4.92e-216	4.92e-216	2.13e-216	1.40e-216

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RESULT
ID QQ
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Best Local S
Matches 18
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ULT 2
Q68020 PRELIMINARY;
Q68020;
Q1-NOV-1996 (TREMBLREL 0
Q1-NOV-1996 (TREMBLREL 0
Q1-NOV-1998 (TREMBLREL 0
                                                                          ULT 3
Q89597
PRELIMINARY;
Q89597;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-PATIENT CASTAG-1'85;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85291; G736119; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24336 MW; E0E4C243 CRC32;
SEQUENCE FROM N.A.
STRAIN-SUB-TYPE AN
                                                    HBCAG.
HEPATITIS
                                         VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 208
                                                                                                                                                                                                                                                                   LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 176
                                                                                                                                                                                                                                                                                  LCWGDLMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 148
                                                                                                                                                                                                                                                                                                                SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 116
                                                                                                                                                                                                                                                                                                                              GMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 88
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                                        RETROID VIRUSES;
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                                                    B VIRUS
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llarity 98.9%;
Conservative
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larity 99.5%;
Conservative
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10°,
                                         HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                          LAST
LAST
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Pred. No. 1.37e-218;
2; Mismatches 0;
                                                                                                  CREATED)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 9.01e-219;
1; Mismatches 0;
                                                                                                                         PRT;
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                                                                          SEQUENCE UPDATE)
ANNOTATION UPDATE)
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Best Local Similarity
Matches 182; Conser
                                   SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ EMBL; X885289; G736113; --
EMBL; X885289; G736113; --
EMBL; X80925; E198085; --
FFAM; PF0906; Hepatitits_core; 1
SEQUENCE 183 AA; 21102 MW; 0C504D47 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KARAYIANNIS P.;
SUBMITED (SEP-1995) TO EMBL/GENBANK/DDBJ
EMBL; X72702; G288930; -
EMBL; X80925; E198084; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24336 MW; 575D20BF CR
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KARAYIANNIS P.;
SUBMITTED (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PATIENT CASTAA-2'87;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of hepatitis negative infection."; ARCH. VIROL. 133:385-396(1993).
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PREISLER-ADAMS S.,
RASENACK J.;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  SUBMITTED (DEC-1995)
                                                                                                                                                                                                                                                                               KARAYIANNIS P.;
                                                                                                                                                                                                                                                                                                       STRAIN-AYW;
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VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                                                                                          KARAYIANNIS P.;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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ilarity 98.9%;
Conservative
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76.48;
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Pred. No. 1.37e-218;
2; Mismatches 0;
Score
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575D20BF CRC32;
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                                          CRC32;
В
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Best Local
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Matches
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067876;
01-NOV-1996
01-NOV-1996
01-NOV-1998
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01-NOV-1996
01-NOV-1998
X, PREC AND
                                                            PRE C/C ORF.
HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
SEQUENCE FROM N.A.
STRAIN-PATIENT CI, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-PATIENT FERRACUTI-1'89;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA I
EMBL; X85284; G736098; -
BFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 183 AA; 21102 MW; BBE9AFBB CRC32;
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Similarity 99.5%;
182; Conservative
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3 (TREMBLREL.
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(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
C GENES (FERRACUTI 1).
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Conservative
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                                                                  HEPADNAVIRIDAE;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.09e-218;
1; Mismatches 0;
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Mismatches 0;
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Q68066;
Q68066;
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011884;
01-JUL-1997;
01-JUL-1997;
01-JUL-1998;
01-NOV-1998;
   HEPATITIS B
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                              5 (TREMBLREL. 01, C
5 (TREMBLREL. 01, L
3 (TREMBLREL. 08, L
C GENES (LICHERI
   VIRUS
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SEQUENCE FROM N.A.

RAO B.S., CASEY J.L., RINAUDO J.

RAO B.S., CASEY J.L., RINAUDO J.

SUBMITTED (MAR-1997) TO EMBL/GEN

EMBL; U95551; G2182120; -.

PFAM; PF00906; Hepatitis_core; 1

SEQUENCE 212 AA; 24360 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CORE ANTIGEN PRECURSOR.
HEPATITIS B VIRUS.
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EMBL; X65258; G59466; -.
PFAM; PF00906; Hepatitis core;
SEQUENCE 212 AA; 24348 MW;
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l Similarity 98.9%;
l82; Conservative
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larity 98.9%;
Conservative
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01, CREATED)
01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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Pred. No. 2.09e-218;
2; Mismatches 0;
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Pred. No. 3.18e-218;
2; Mismatches 0;
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DATA BANKS
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268025
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LAIM M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA B EMBL; X85315; G736207; -...

PFAM; PF00906; Hepatitis_core; 1.

SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;
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HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE;
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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STRAIN-PATIENT LICHERI-2'87;
LAI M.E., MAZZOLENI A.F., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
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Local Similarity 98.9%;
les 182; Conservative
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Pred. No. 7.37e-218;
3; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                      Score 1370; DB 14; Pred. No. 7.37e-218;
PRT;
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6F38AA3B CRC32;
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Best Local Similarity 98.9%;
Matches 182; Conservative
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Best Local
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067872;
01-NOV-1996
01-NOV-1998
01-NOV-1998
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01-NOV-1996
01-NOV-1996
01-NOV-1998
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PRE-C/CORE.
HEPATITIS E
                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-PATIENT C, HBSAG POSITIV, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELLS A., P
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X65257; G59431; -.
EMBL; X65257; G59431; -.
EPAM, PFO0906; Hepatitis—core; 1.

SEQUENCE 212 AA; 24348 MW; A6BD9DA1 CRC32;
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HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-PATIENT CASTAG'3;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X85293; G736126;
EMBL; X85293; G736126;
SEMBL; X85293; G736126;
SEMBL; X85293; G736126;
SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;
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                  177
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Local Similarity 98.4%;
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ESQC
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                   VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
                                     VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
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                                                                                                                                      181;
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RETROID VIRUSES;
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(TREMBLREL.
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10°,
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LAST SEQUENCE LAST ANNOTED
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Pred. No. 7.37e-218
1; Mismatches 1
                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                     Score 1369; DB 14;
Pred. No. 1.12e-217
2; Mismatches 1
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ANNOTATION UPDATE)
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Best Local
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PRE-C/CORE.
HEPATITIS B
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q68032;
Q68032;
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LIMIM.E., WAZZOLENI A.P., PORRU A., BALESTRIERI A.; SUBMINITED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85256; G736052; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24322 MW; 83D9780B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q67984
Q67984;
                                                                                                                                                                                                                                                                                                                                                          EMBL; X85296; G736139; -
PFAM; PF00906; Hepatitis_core;
SEQUENCE 212 AA; 24308 MW;
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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01-NOV-1998 (TREMBLREL.
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HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
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                                                                                                                                                                                                                           Score 1369; DB 14;
Pred. No. 1.12e-217;
3; Mismatches 0;
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LAST SEQUENCE UPDATE)
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Pred. No. 1.12e-217;
1; Mismatches 1;
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STRAIN-PATIENT GIORDO'84;
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SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E
EMBL; X85316; G736210; -
FPAM: PF00906; Hepatitis_core; 1.
SEQUENCE 7. 212 AA; 24376 MW; 80F52D0F CRC32;
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STRAIN-PATIENT FERRACUTI-2'90;

LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;

SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; X85285; G736100; ...

PFRAM, PF00906; Hepatitis_core; 1.
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1 Similarity 98.4%;
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212 AA; 24292 MW; 04
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larity 98.9%;
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Score 1366; DB 14;
Pred. No. 3.96e-217;
1; Mismatches 1;
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Pred. No. 1.71e-217;
2; Mismatches 1;
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LAST SEQUENCE UPDATE)
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BANKS
                                                                   Length 212;
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   Gaps
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Dec 16 13:20:19 1999; MasPar time 12.84 Seconds 460.333 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score:

>US3869-29-38183 (1-278) from us3869-29-38183.pep 2088 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 278

Scoring table: РАМ 150 Gap 11 Sequence:

Searched: 170751 segs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 33.381; Variance 171.697; scale 0.194

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

11111111111111111111111111111111111111	Result
1375 1375 1363 1369 1359 1349 13449 13384 13384 13334 13334	Score
55555555555555555555555555555555555555	Query
194 3412 1193 1193 1183 1183 1183 1183 1183 1183	Length DB
32 32 32 33 32 32 32 32 32 32 32 32 32 3	BG
W50242 W50250 W50250 W50250 W50251 W50241 W50241 W50244 W69044 R05635 R05635 R40806 R40806 R40806 R40806	ID
Hepatitis B virus pre Hepatitis B virus pre S12/core protein. Hepatitis B virus sub Hepatitis B virus pre Hepatitis B virus pre Hepatitis B virus pre Hepatitis B virus core Hepatitis B antigen. Sequence of core anti Plasmid phBv DN AA en Sequence of core anti Plasmid phBv DN AA en Sequence of core of core Hepatitis B core / pv Hepatitis B core / pv Hepatitis B core prot Hepatitis B core prot	Description
1 04e 100 1 04e-100 1 04e-100 1 02e-99 2 18e-99 2 18e-99 6 84e-99 6 84e-99 1 47e-98 1 47e-98 3 80e-97 1 44e-97 2 55e-97 2 55e-97	Pred. No.

133 63.8 198 8 R40807 Hepatitis B virus cor 1325 63.5 234 1 P90702 Deduced amino acid see 1325 63.5 214 1 P90702 Deduced amino acid see 1325 63.5 214 1 P90702 Deduced amino acid see 1325 63.5 289 20 W09049 Plasmid pHBV DN BB en 1324 63.4 185 6 R30780 Native HBcAg protein 1324 63.4 185 6 R30780 Native HBcAg protein 1324 63.4 185 6 R31025 Native HBcAg protein 1324 63.4 185 6 R31025 Native HBcAg protein 1324 63.4 185 6 R31025 Hepatitis B virus pol 1320 63.2 183 13 R68869 Hepatitis B virus pol 1317 63.1 185 6 R30781 Altered HBcAg protein 1317 63.1 185 6 R30781 Altered HBcAg protein 1314 62.9 183 13 R68867 Hepatitis B virus pol 1311 62.8 185 6 R31025 Hepatitis B virus pol 1311 62.8 185 6 R30784 Altered HBcAg protein 1311 62.8 185 6 R30784 Altered HBcAg protein 1308 62.6 185 6 R30783 Altered HBcAg protein 1308 62.6 185 6 R30862 Hepatitis B virus pol 1287 61.6 198 32 M50252 HBCAg protein 1308 62.4 214 1 P80961 HBCAg protein 1308 62.4 214 1 P80961 HBCAg protein 1308 62.5 183 17 R98883 Hepatitis B virus E a 1258 60.2 183 17 R98884 Hepatitis B virus E a 1258 60.2 183 17 R98884 Hepatitis B virus E a 1258 60.2 183 17 R98884 Hepatitis B virus E a 1258 60.2 183 17 R98884	45	44	43	42	41	40	39	38	37	36 6	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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R68866 Hepatitis B virus co R55286 PreSI full length co R55286 PreSI full length co R55286 PreSI full length co R55286 PreSI full length co R56866 Hepatitis B virus po R55284 Plasmid pHBV DN BB e R30780 Native HBcAg protein R30781 Core antigen of HBV. R68867 Hepatitis B virus po R68867 Hepatitis B virus po R68867 Hepatitis B virus po R68867 Hepatitis B virus po R68870 Altered HBcAg protei R30784 Altered HBcAg protei R30784 Altered HBcAg protei R30785 Altered HBcAg protei R30862 Hepatitis B virus po R68970 Altered HBcAg protei R30862 Altered HBcAg protei R30863 Altered HBcAg protei R30783 Altered HBcAg protei R30864 HBCAg/beta-Gal Fusic P80961 HBV core antigen end R308878 Hepatitis B virus E R308883 Hepatitis B virus E R308884 Hepatitis B virus E	83	83	83	86	$\vdash$	0	œ	æ	8	œ	œ	œ	œ	83	83	œ	85	83	85	œ	85	85	œ	9	$\vdash$	83	93	9	ü
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expression vectors and host cells. They can be provided exogenously	District Specifical teachers of periods of teachers	rted into the p22 and Met-p22 polypeptides. The	W50238) Heterologous pentides (see W50244-49) may be	, p18 (see W50236), Met-p18 (see W50237) and Me	itable inhibitory proteins include p25 (see W50	of them, leads to transdominant inhibition	Thus, over-expression of the precore prote	끍	(see W50251), which is the usual nucleocapsid component, and	incorporated into HBV nucleocapsids along with the p21 core protein	HBV precore or precore-related proteins. These proteins can be	that HBV replication is inhibited in the presence of high levels of	ښي	elimination of the 19-amino acid leader peptide from the 25 kDa	protein with an added N-terminal Met residue. p22 is produced by	This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)		f viral replication, especially hepatitis B vir	leocapsid subunit(s) into a viral nucleocapsid - usefu	DNA encoding proteins which can be incorporated with wild type	325/17.	Melegari M, Scaglioni PP, Wands JR;			••	12-MAR-1998.		/label- p22	Protein 2194	Key Location/Qualifiers	Synthetic.	virus.	; Met-p22.	lication; inhibitor; HBV; nucleocapsi	virus pr	-1998 (first entry)	WSO242 STREETER, FINCEIR, INT. ST.	TOOM I

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                                                                                                                                                 DRA encoding proteins which can be incorporated with wild type or nucleocapsid subunit(s) into a viral nucleocapsid - useful for protein in the isence of viral replication, especially hepatitis B virus protein in the isence of high levels of HBV replication is inhibited in the isence of high levels of HBV precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsid along with the p21 core protein (see W50251), which is the usual nucleocapsid component, and thereby render the nucleocapsid deficient in encapsidating HBV precore of HBV replication. Suitable corpression of the precore proteins, or certain variants of them, corpression of the precore proteins, or certain variants of them, corpression of the precore proteins, or certain variants of them, corpression of the precore proteins and thereby replication. Suitable combinant inhibition of HBV replication. Suitable combinant proteins include p25, p22 (see W50241), Met-p18 (see W50237) and wet-p18 Het core combinant methods using claimed expression vectors and host crecombinant methods using claimed expression vectors and host construct that directs overexpression of an inhibitory protein in construct that directs overexpression of an inhibitory protein in construct that directs overexpression of HBV infection.
                                                                         Matches
                                                                                         Query Match
Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the target cells for use in inhibiting HBV replication. Alternatively, a nucleic acid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.

Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-1997; U15500.

03-SEP-1996; US-025370.

(GEHO ) GEN HOSPITAL CORP.

Melegari M, Scaglioni PP, Wands JR;

MPI: 98-193325/17.
; 95, SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatocyte; liver; p25 protein.
Hepatitis B virus.
W09809649-Al.
12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus precore p25 polypeptide.
Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
                                                                                                                                           Sequence
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                                                                                       Score 1375; DB 32; Pred. No. 1.04e-100;
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Pred. No. 1
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L.04e-100;
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                                                                                                                                                                                             PT Vaccine complies recombinant, attenuated pox-virus - use for PT Vaccinating against viral infections such as rables, hepatitis B, PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

PT Disclosure
Query Match
Best Local S
Matches 18
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207-MAR-1991; US-666056.

211-JUN-1991; US-713967.

3 06-MAR-1992; US-847951.

4 (VINO-) VIROGENETICS CORP.

5 (COX WI, De Taisne C, Francis J, Gettig RR, Johnson GP, Limbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus SE, Riviere M, Tartaglia J, Taylor J;

6 Riviere M, Tartaglia J, Taylor J;

7 Riviere M, Tartaglia J, Taylor J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-FEB-1993 (first entry)
$12/core protein.
$12/core protein.
Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
vaccinia virus; 13L; promoter; NVVAC; recombinant; HBV L;
large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;
$1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R27473 standard; Protein; R27473;
                                                                                                                                                                       vaccinia genome and would Q35501-864.
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larity 99.5%;
Conservative
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109..163
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164..346
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                                1375; DB 5;
No. 1.04e-100;
                                                                 Length 346;
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Similarity

163 nmdidpykefgatvellsflpsdffpsvrdlldtasalyrealespehcsphhtalrqai 222

Mismatches

0;

Gaps

0

28-SEP-1998

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RESULT PRO CHEST PRO
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PF 07-DEC-1987; US-106538.

PR 07-CCT-1987; US-939517.

PA (SCRI-) Scripps Clinic Res.

PI Thornton GB, Moriarty AM, Millich DR, McLachlan A.;

PA (SCRI-) Scripps Clinic Res.

PI Thornton GB, Moriarty AM, Millich DR, McLachlan A.;

PA (SCRI-) Scripps Clinic Res.

PI Thornton GB, Moriarty AM, Millich DR, McLachlan A.;

PA (SCRI-) Scripps Clinic Res.

PI Thornton GB, Moriarty AM, Millich DR, McLachlan A.;

PA (SCRI-) Scripps Clinic Res.

PI Thornton GB, Moriarty AM, Millich DR, McLachlan A.;

PA (SCRI-) Scripps Clinic Res.

PI Row Conjugates and fusion proteins of immunogenic polypeptide -

PT and hepatitis B core antigen, useful in vaccines.

PT and hepatitis B core antigen, useful in vaccines and cand acid corresponding to the above mentioned HBV regions are T cell

PS Disclosure; p: English.

CC e.g. by using a bifunctional reagent which forms a disulphide link, useful response to HBcAg in infected

CC cunharcre
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
LT 5
W50241 standard;
W50241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
EP-271302-A.
                                                                                                                                                                                                                                                                                                                                                            subjects.
See also P80896-P80898 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus subtype ayw. core protein.
Conjugate; fusion protein; hepatitis B core protein; HBV subtype ayw.;
T cell stimulating polypeptide; vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P80959 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1990 (first entry)
                                                                                                                          215
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                                                                                                                                                                             CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTF-GRETVIEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL 155
                                                                                                                                                                                                                                                                                           l Similarity
183; Conser
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             Protein;
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Pred. No. 1.02e-99;
0; Mismatches 0.
             B
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                                                                                                                                                                                                                                                                                                                   Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT DNA encoding proteins which can be incorporated with wild type
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT inhibition of viral replication, especially hepatitis B virus
PS Claim 9; Page 34-55; 6(pp; English.

CC protein that is produced by elimination of the 19-amino acid leader
CC protein that 25 kDa full-length HBV precore protein (see
CC w50250). Evidence is provided that HBV precore protein (see
CC proteins. These proteins can be incorporated into HBV nucleocapsids
CC along with the p21 core protein (see W50251), which is the usual
CC nucleocapsid component, and thereby render the nucleocapsids
CC along with the p21 core proteins (see W50251), which is the usual
CC nucleocapsid component, and thereby render the nucleocapsids
CC expression of the precore proteins, or certain variants of them,
CC expression of the proteins of HBV pregnomic RNA. Thus, over-
CC expression of the proteins of HBV preplication. Suitable
CC inhibitory proteins include p25 (see W50250), p22, Met-p22 (see
CC w50242) p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
CC (see W50238). Heterologous peptides (see W50237) and Met-p18-Het
CC (see W50238). Heterologous peptides (see W50244-49) may be
clisserted into the p22 and Met-p25 polypeptides. The inhibitory
CC proteins can be produced by recombinant methods using claimed
construct that directs overexpression
CC Alternatively, a nucleic acid construct that directs overexpression
CC of an inhibitory protein in target cells is used for the gene
           SULT

W50251;
W50251;
W50252;
C28-SEP-1998 (first entry)
E Hepatitis B virus p21 core protein.
W Viral replication; inhibitor; HBV; nucl.
W hepatocyte; liver; p21; core protein.
W Hepatitis B virus.
W Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 181; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1997; U15500.
03-SEP-1996; US-025370.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, WMPI; 98-193325/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus precore p22 polypeptide. Viral replication; inhibitor; HBV; nucleoc hepatocyte; liver; p22 protein. Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9809649-A1.
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                                                                                                                                                                                                                                                                                                                                                                                          lcwgelmtlatwvgvnledpasrdlvvsyvdtnmglkfrqllwfmiscltfgretv1eyl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gmdidpykefgatvellsflpsdffpsvrdlldtasalyrealespehcsphhtalrqa1
                                                                                                                                                                                                                                                                                               VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
                                                                                                                                                                                                                                                                                                                                                                       LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection.
Location/Qualifiers
72..88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1359; DB 32;
Pred. No. 2.18e-99;
2; Mismatches 1;
                                                                       nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleocapsid; gene therapy;
                                                                       gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 193;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prinhibition of viral replication, especially hepatitis B virus
prinhibition of viral replication, especially hepatitis B virus
CC This is the 21 kDa (p21) protein of hepatitis B virus (HBV) that
CC assembled into a 180 kSa subunit nucleocapsid structure that
promotes viral replication. Fridence is provided that HBV
CC replication is inhibited in the presence of high levels of HBV
CC replication is inhibited in the presence of high levels of HBV
CC replication is inhibited in the presence of high levels of HBV
CC incorporated into HBV nucleocapsids deficient in encapsidating HBV
CC incorporated into HBV nucleocapsids deficient in encapsidating HBV
CC replication. Suitable inhibitory proteins include p25 (see
CC replication. Suitable inhibitory proteins include p25 (see
CC replication. Suitable inhibitory proteins include p25 (see
CC w50350), p22 (see w50241), Met-p22 (see w50242), p18 (see w50235),
CC can be produced by recombinant methods using claimed expression
CC can be produced by recombinant methods using claimed expression
CC cells for use in inhibiting HBV replication. Alternatively, a
CC culcic acid construct that directs overexpression of an inhibitory
CC protein in target cells is used for the gene therapy of HBV
CC consecuence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Ma
Best Loc
Matches
                              misc_difference
                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus core protein.

Hepadhavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus; ground squirrel hepatitis B virus; duck hepatitis B virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09044 standard; Protein; 183
W09044;
11-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding proteins which can be incorporated with wild type nucleocapsid subunit(s) into a viral nucleocapsid - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9809649-A1.
12-MAR-1998.
03-SEP-1997; U15500.
03-SEP-1996; US-025370.
                                                                                                                                                                                                                                                                                                                        Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                         core
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                                                                                                                                                                                                                                                                                                                                                      protein;
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                                                                                                                                                                                                                                                                                                                                                   replication; antiviral;
                                                                                                                                                                                                                                                               Location/Qualifiers 71..180
                                                                                                                                                   polypeptides
81..180
                                                                                                                                                                     /note= "C-terminus of core protein is at any acid position between 71-180 in mutant polypeptides of the invention (Claim 23)"
                                 polypeptides
171..180
                                                                                       acid position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                     /note=
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98.9%;
                                                   "C-terminus of core protein is at a sition between 81 and 180 in mutant ptides of the invention (Claim 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "immunodominant region"
   "C-terminus
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Pred.
1; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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No. 2.64e-99;
of core protein is at
                                                                                                                                                                                                                                                                                                                                                      gene
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Matches
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09-JAN.1997.
20-JUN.1996; U10602.
20-JUN-1995; US-017814.
(GEHO) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
WPI: 97-087176/08.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 55-56; 83pp; English.

Alteration of the C-terminus of the core protein (W09044) of hepatitis B virus (HBV) or other hepadnavirus creates a mutant polypeptide capable of reducing replication of the wild-type virus of dominant negative mechanism. The inhibitory effect is species-specific and is achieved by deletion of a few C-terminal amino acids from the core protein, and/or by joining the core protein to a hepadnavirus surface protein (see also W09045), creating a core-surface fusion. Such mutant polypeptides (see also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
                                                        R05635 standard; protein; 183
R05635;
30-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New method for inhibiting the replication of hepadnaviruses -
comprises introducing a mutant polypeptide with a mutated core
protein or corresponding nucleic acid, for treating, e.g. hepatitis
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181; Conser
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                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminus of core protein is at any acid position between 174 and 180 in mutant polypeptides of the invention (Claim 26)" 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       position 178 in mutant invention (Claim 7) " 172..183
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174..180
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178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid position between 171 polypeptides of the invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminus of o
position 178 in mutant
invention (Claim 7)"
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                                                                                                                                                                                                                                                                                                                               64.8%;
98.9%;
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                                                                                                                                                                                                                                                                                                                    Score 1353; DB 20;
Pred. No. 6.84e-99;
0; Mismatches 2;
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(Claim
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  Query Match 64.6%;
Best Local Similarity 96.7%;
Matches 177; Conservative
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22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
(BIO) Biogen Inc.
Murray K, Schaller HE;
WPI; 90-195067/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1980.
21-DEC-1979;
22-DEC-1978;
22-DEC-1978;
01-NOV-1979;
                                                                                         Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Example; Figs 3-4; 43pp; English.

Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contg. pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBY-G-L, e.g. E. coli HB101/pBR322-PSt I dG: HBY-Kpn I dC: Tetr AmpS HBY+.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HBV and may be used as a vaccine or in detect cultured in a suitable bacterial host such Fragments of the sequence are also claimed useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of core antigen. Hepatitis B virus; antigen; antibody; diagnosis; vaccine. Hepatitis B virus.
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Polypeptide fragments encoded by th
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Murray K, Schaller HE;
WPI; 80-57268C/33.
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177; Conser
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GB-050039.
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96.7%;
Score 1349; DB 5;
Pred. No. 1.47e-98;
5; Mismatches 1
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Pred. No. 1.47e-98;
5; Mismatches 1
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                                                                                                                           Query Match
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Matches 17
                                                                                                                                                                                                            plasmid phBv DN AA carries an insert (T49598) coding for a prot (W09048) comprising a hepatitis B virus (HBV) core protein (see also W09049) at amino acid 179 with the HBV surf protein (see also W09045) at amino acid 8. Plasmid phBv DN BB (T49599) expresses the HBV core fused at amino acid 175 to the surface protein at amino acid 112 (W09049). HBV DN AA was at least as potent an inhibitor of HBV replication as construct pHBV DN (T49597); phBV DN BB was less inhibitory than pHBV DN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pHBV DN AA encoded HBV dominant negative polypeptide. Hepadnavirus; woodchuck hepatitis virus; hepatitis delta viru HBV; ground squirrel hepatitis B virus; duck hepatitis B virus core protein; replication; antiviral; gene therapy; pHBV DN A Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                        N-PSDB; T49598.

New method for inhibiting the replication of hepadnaviruses comprises introducing a mutant polypeptide with a mutated core protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 10
W09048
                                                                                                                                                                          Vectors expressing hepadnavirus dominant negative core mutants be utilised in the gene therapy of viral infections. Sequence 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1996; U10602.
20-JUN-1995; US-017814.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09048;
11-APR-1997
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 46-48; 83pp; English.
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                           CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
                                       cwgelmtlatwvgvnledpasrdlvvsyvntnmglkfrqllwfhiscltfgretvieylv
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                                                                                                                       ch 64.4%;
1 Similarity 100.0%;
179; Conservative
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180..397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= HBV_core
/note= "positions
1-179 of HBV core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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9-226 of HBV
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Pred.
0; M
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1. No. 3.80e-98;
Mismatches 0;
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DN AA.
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Matches 17
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21-DEC-1979; 303017.
22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA coding for polypeptide - have specificity of hepatikis B viral antigens in detection or antibody stimulation Claim 13; Page 40; 43pp; English. Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contg, pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dG:
  J05192170-A.
03-AUG-1993; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS LTD.
                                                                                                                                                                                                                                               Hepatitis B core / PV-1 Hepatitis B; core; HBC; Synthetic.
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Murray K, Schaller HE;
WPI; 80-57268C/33.
N-PSDB; N00002.
                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                             R40806;
16-FEB-1994
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R40806 standard; Protein; 196
                                                                                                                                                       protein
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177; Conservative
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core; HBC; PV-1; I
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                                                                                                                             /label=
14..196
/label=
                                                                                                                                                                                                                           Location/Qualifiers
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96.2%;
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Pred. No. 1.19e-97;
5; Mismatches 1.
                                                                                                                                                                                                                                                                               IL-1 beta;
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RESULT 13

ID R40808;

R40808;

AC R40808;

DT 16-FEB-

DE Hepatit

KW Hepatit

KW Hepatit

KW Hepatit

KW Hepatit

FT region

FT region

FT J051921

PD 03-AUG-
PF 24-SEP-
PF 24-SEP-
PA (NISW)

DR WPI; 93

DR WPI; 93

DR N-SDB;

PT Recombi

PT virus a

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Best Local Similarity
Matches 175; Conser
                                                                            Matches
                                                                                        Query Match
Best Local :
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24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILL
WPI; 93-277479/35.
N-PSDB; Q47738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant plasmid for high immunogenity virus - contains recombined haemagglutinin gene, hepatitis B core gene of vaccir virus and exotic genes

Disclosure; Fig 7; 12pp; Japanese.

The hepatitis B core gene is recombined with PV-1 DNA and IL-1 beta to form a plasmid (Q47738) which is then used to a vaccine. NB: Sequence is difficult to read in the original
                                                                                                                                                    Recombinant plasmid for high immunogenity virus - co recombined haemagglutinin gene, hepatitis B core gen virus and exotic genes Disclosure; Fig 9; 12pp; Japanese.

The hepatitis B core gene is recombined with pv-1 DN and IL-1 beta to form a plasmid (Q47738) which is the a vaccine. NB: Sequence is difficult to read in the
                                                                                                                             specification.
Sequence 208
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Hepatitis
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N-PSDB; Q47736.
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ilcwgelmnlatwvgsnledpasrelvvsyvnvnmglkirqllwfhiscltfgretvley 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
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core / PV-1 / IL-1 Fusion.
core; HBC; PV-1; IL-1 beta;
                                                                           64.0%;
parity 94.6%;
Conservative
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26..208
/label= HBC
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/label- pv-1
20..25
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95.1%;
                                                                                                                                                                                                                                                                           MILLS
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Pred. No. 1.
6; Mismatc
                                                                           Score 1337; DB 8;
Pred. No. 1.44e-97;
7; Mismatches 3
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1.74e-97;
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                                                                                                    Length 208;
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Best Loc
Matches
Hepatitis B core protein.

Hepatitis B; core; HBC; PV-1; IL-1 beta; int.
Hepatitis B Virus.
J05192170-A.
03-AUG-1993.
24-SEP-1991; J243800.
24-SEP-1991; JP-243800.
(NISW) NISSHIN OIL MILLS LTD.
WPI; 93-277479/35.
N-PSDB; Q47735.
Recombinant plasmid for high immunogenity virus and exotic genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE) TAKEDA CHEMICAL IND KK.

WPI; 84-143231/23.

DNA used in prevention of infections by hepatitis virus B -
comprises structural gene of hepatitis virus adr B surface antigen
coding gene and at least 1 virus core antigen structural gene.
Disclosure; Fig 3; 13pp; Japanese.

The sequence is that of hepatitis virus core antigen (HBcAg). It
can be used as a vaccine for the prevention of infections by
hepatitis B virus (HBV) and also in the diagnosis of early stages
of HBV infection. See also P40310.
                                                                                                                                                                                                                                                                                                                                 T 15
R40805 standard; Protein;
R40805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBCA9; vaccine; diagnosis; HBV infection. Hepatitis b virus. J59074985-A. 27-APR-1984. 19-OCT-1982; 183432. 19-OCT-1982; JP-183432.
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P40311 standard; Protein;
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18-AUG-1992 (first entry)
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Local Similarity 95.6%;
es 175; Conservative
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Pred. No. 2.55e-97;
5; Mismatches 3;
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                             B core
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                                                                                                                                              Query Match
Best Local S
Matches 17
                                                                                                                                                                                        Disclosure; F1g 6; 12pp; Japanese.
The hepatitis B core gene is recombined with PV-1 DNA
and IL-1 beta to form a plasmid (Q47738) which is then used to produce
a vaccine. NB: Sequence is difficult to read in the original
specification.
                                                                                                                                                                                   Sequence
276
                  181
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                sqc 183
                                                                        CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
                                                                                                                                              l Similarity
175; Conse
                                                                                                                                                                                   183 AA;
                                                                                                                                             63.9%;
llarity 95.6%;
Conservative
                                                                                                                                             Score 1334; DB 8; L. Pred. No. 2.55e-97; 5; Mismatches 3;
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Search completed: Thu Dec 16 13:23:42 1999 Job time: 203 secs.

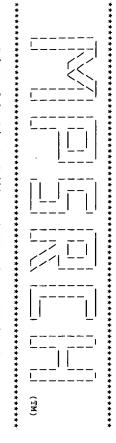
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US3869-29-38183
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MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESP
DGFLLLOMDFGFPEHLLVDFLQSLSMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESP
EHCSPHHTALRQAILCWGELMTLATWVCYNLEDPASRDLVVSYYWTNMGLKFRQLLWFHISCLTFGRETV
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:23:59 1999; MasPar time 13.87 Seconds 803.274 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

>US3869-29-38183 (1-278) from us3869-29-38183.pep 2088 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 278

Scoring table: PAM 150 Gap 11

Searched:

122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 46.997; Variance 115.318; scale 0.408

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1.36e-198	.18e-19	6.19e-199	.19e-19	.18e-1	.82e-1	2.82e-199	ù	1.90e-199		8.64e-200	5.82e-200	1.79e-200	1.79e-200	1.20e-200	1.20e-200	4	.47e-	1.13e-201	1.13e-201	5.14e-202	

##ccession S53234 #accession S53234 ##molecule_type DNA ##residues 1-2 ##cross-references: ##ccession S53264 ##accession S53264 ##molecule_type DNA ##residues 1-2: ##cross-references:	##CCESSION 53191  ##molecule_type_DNA ##residues 1-2  ##cross-references  ##experimental_sour ##experimental_sour 53209  ##accession 53209  ##molecule_type_DNA ##residues 1-2  ##cross-references ##experimental_sour ##experimental_sour	San a	REFERENCE #authors #submission #description	DATE ACCESSIONS	RESULT 1 ENTRY TITLE ALTERNATE_NAMES CONTAINS ORGANISM #variety
ce isolate patient 12 ##label LA3 12 ##label LA3 ce isolate patient 12 ##label LA4 EMBL:X85313; NID:g	##molecule_type_DNA ##rcsidues 1-212 ##label_LAI ##rcross-references_EMBL:X85283; NID:g736088; PID:g736090 ##experimental_source_isolate_patient_Ferracuti'83 cession S3209 ##molecule_type_DNA ##molecule_type_DNA ##residues 1-212 ##label_LA2 ##cross-references_EMBL:X85290; NID:g736114; PID:g736116 ##cross-references_EMBL:X85290; NID:g736114; PID:g736116	##molecule_type_DNA ##residues 1-212 ##label PLU ##residues 1-212 ##label PLU ##cross-references EMBL.235716; NID:g527435; PID:g527437 ##experimental_source subtype ayw4, 1solate hb321 #RESTANCE SS3112 thors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A. bmission submitted to the EMBL Data Library, March 1995	S03/// NO3/II \$47404  Plucienniczak, A.  Submitted to the EMBL Data Library, August 1994  Molecular cloning and sequencing of two complete genomes of polish isolates of human hepatitis B virus.	isolate 85; isola on 08-Nov	complete or / core and isolate hbs: rsor / HBC intigen titis B vire late hb321;

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30-178
                  #variety
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#accession A03711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
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##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
##experimental_source isolate patient Licheri'83
##experimental_source isolate patient Licheri'83
                                                                                                                                                                                                275
                                                                                                                                                                                                                                                                 ##cross-references GB:J02203; NID:g329640; PID:g329642
##experimental_source subtype ayw
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##experimental_source patient Giordo-2'86
##note due to a stop codon between the alternative initiators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:X85306; NID:g736172; PID:g736174 ##experimental_source isolate patient Flore-1'86 :cession S53262
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Similarity 99.5%;
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alternative initiators; core protein
                                                                     HBc antigen
                                                                                      core antigen -
Castaa-2'87)
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Galibert, F.; Mandart, E.;
#formal_name hepatitis B virus, HBV
isolate patient Castaa-2'87
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                           S53207
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Nature (1979) 281:646-650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #length 212
                                                     core antigen
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                                                                                                                     #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #molecular-weight 24350
                                                                                                      hepatitis B virus (isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1375; DB 1;
Pred. No. 4.25e-205;
1; Mismatches 0;
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                                                                                                                                                                                                                                       ##residues 30-212 ##label LAW ##cross-references EMBL:X85284; NID:g736095; PID:g736098 ##cross-references EMBL:X85284; NID:g736095; PID:g736095; PID:
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##experimental_source isolate patient Castaa-2'87
##note due to a stop codon between the alternative initiatiors
the e antigen precursor cannot be produced
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##residues 1-183 ##label LAI
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$53112
Lai, M.E.; Ma:
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$53112
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#formal_name hepatitis B virus, HBV
isolate patient Castag-1'85; isolate patient Ferracuti-1'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
cs-271.cs-2707
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HBc antigen; HBe antigen precursor / HBc antigen;
                                                                                                                          *superfamily hepatitis B virus core antigen alternative initiators; core protein
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#superfamily hepatitis B virus core antigen
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llarity 99.5%;
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Pred. No. 9.36e-205;
1; Mismatches 0;
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Data Library, March 1995
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                 LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 148
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#superfamily hepatitis B virus
core protein
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HBe antigen precursor / HBC antigen;
core antigen; e antigen
efformal_name hepatitis B virus, HBV
subtype ayw, patient C1000

20-Feb_1995 *sequence_revision 20-Feb
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##experimental_source subtype ayw, patient CI
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                                                                                                                                                     ESQC
                                                                                                                                                                                                                            VAFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 208
                                                                                                                                                                                                                                                                  LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 214
                                                                                                                                                                                                                                                                                                                       SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 154
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1 Similarity 98.9%;
182; Conservet
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HBe antigen precursor / HBc antige core antigen; e antigen artigen beformal_name hepatitis B virus, H subtype ayw, patient CI 20-Feb-1995 #sequence_revision 20 08-Sep-1997
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Sequence analysis of HBV genomes isolated
HBSAg negative chronic liver disease.
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e anti
#formal_name hepatitis B virus,
isolate patient Licheri-2'87
08-Jul-1995 #sequence_revision ()
                                           core antigen
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Licher1-2'87)
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alternative initiators; core protein
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                                                                                #type complete
en - hepatitis |
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recursor / core antigen -
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Pred. No. 9.36e-205;
2; Mismatches 0;
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Query Match 65.6%;
Best Local Similarity 98.9%;
Matches 182; Conservative
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##cross-references EMBL:X85314; NID:g736201; PID:g736204
##cross-references EMBL:X85314; PID:g736201; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-212 ##label LAI
##cross-references EMBL:X85293; NID:g736124; PID:g736126
##experimental_source isolate patient Castag'3
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$53270
$53112
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HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen

#formal_name hepatitis B virus, HBV
isolate patient Castag'3

08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                  *superfamily hepatitis B virus core antigen alternative initiators; core protein
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llarity 98.4%;
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                                                                                                                          #length
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212 #molecular-wain
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Score 1370; DB 2; 1
Pred. No. 3.06e-204;
1; Mismatches 1;
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Pred. No. 3.06e-204;
3; Mismatches 0;
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Data Library, March 1995
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Best Local :
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                                                                                                                         215 VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA #residues 1-212 ##Label LAI #residues 1-212 ##Label LAI ##residues ##residues ##residues ##residues ##residues ##cyoss-references EMBL:X85315; NID:q736205; PID:q736207 ##cyperimental_source isolate patient Licheri-3'90
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Similarity 98.9%;
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e antigen precursor / core antigen - hepatitis B virus
(isolate patient Licheri-3'90)
HBe antigen precursor / HBc antigen; pre-C/C antigen
core antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate patient Licheri-3'90
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
S53163
e antigen
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S53112
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#domain carboxyl-terminal propeptide #link EAG
predicted #label ECP
gth 212 #molecular-weight 24366 #checksum 446
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#type complete
precursor / core antigen
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to the EMBL
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Pred. No. 3.06e-204;
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Data 1
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Library, March 1995
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                             ##experimental_source subtype ayw,
                                             ##residues 1-212 ##label LAI
##cross-references EMBL:X65257; N
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Similarity 98.9%;
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S HBe antigen precursor / HBc antigen; pocore antigen; e antigen

#formal_name hepatitis B virus, HBV subtype ayw, patient C

20-Feb-1995 #sequence_revision 20-Feb-1908-Sep-1997
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S53163
S53112
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                                                                                                                                                                                                   S20746
S20745
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                                                                                                             submitted to the EMBL Data Library, March 1992
Sequence analysis of HBV genomes isolated from
HBSAg negative chronic liver disease.
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#formal_name hepatitis B virus, HBV
isolate patient Vittorina'92
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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#product core antigen #status predicted #label CAG\
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#domain carboxyl-terminal propeptide #link EAG #status
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Pred. No. 4.53e-204;
1; Mismatches 1;
                                             NID:g59429; PID:g59431
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Best Local :
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##experimental_source isolate patient Chighine-2'86
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 155 LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
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                                                                       SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 154
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Similarity 98.4%;
                                                                                                                                                               55.6%;
Similarity 98.4%;
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HBe antigen precursor / HBc antigen;
core antigen; e antigen
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S53112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name hepatitis B virus, HBV isolate patient Chighine-2'86 08-Jul-1995 #sequence_revision 03-Au 08-Sep-1997
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#product core antigen #status predicted #label CAG\
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#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP
#length 212 #molecular-weight 24348 #checksum 506
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alternative initiators; core protein
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alternative initiators; core protein
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Pred. No. 4.53e-204;
2; Mismatches 1;
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Pred. No. 4.53e-204;
3; Mismatches 0;
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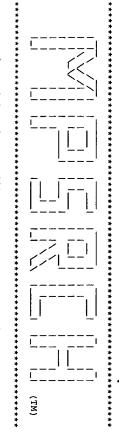
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HBe antigen precursor / HBC antigen;
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HBe antigen precursor / HBc antigen;
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         core antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate patient Chighine-1',85
08-Jul-1995 #sequence_revision 03-Aug-1995
08-Sep-1997
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Pred. No. 6.72e-204;
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Data I
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Library, March 1995
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1-212 ##label LAI
##cross-references EMBL:X85316; NID:g736208; PID:g736210
##cross-references isolate patient patient Glordo'84
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##cross-references EMBL:X85295; NID:g736134; PID:g736136
##experimental_source isolate patient Chighine-1'85
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HBe antigen precursor / HBc antigen;
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isolate patient Giordo'84
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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to the EMBL Data Library, March 1995
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Pred. No. 1.48e-203;
3; Mismatches 1;
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Best Local Similarity 98.4%;
Matches 180; Conservative
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##cross-references EMBL:x85275; NID:g736057; PID:g736060
##experimental_source isolate patient Muresu'89
##note due to a stop codon between the alternative initiations
##note the e antigen precursor cannot be produced
                                                          276
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                                                                                                                  216 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
                                                                                                                                                                                                                                       61 CWGELMTLATWVGANLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV 120
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                                                          278
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core protein
#length 183 #molecular-weight 21088 #checksum 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A. submitted to the EMBL Data Library, March 1995 $53169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name hepatitis B virus, HBV isolate partent Muresu'89 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997
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HBc antigen
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                                                                                                                                                                                                                                                                                                  Score 1364; DB 2;
Pred. No. 3.26e-203;
2; Mismatches 1;
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1; Mismatches 1; Indels
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 16 13:25:14 1999; MasPar time 9.63 Seconds 816.384 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence:

>US3869-29-38183 (1-278) from us3869-29-38183.pep 2088 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 278

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 48.215; Variance 102.691; scale 0.470

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

2221187 32210987 32210987	Result
1374 1348 1349 1336 1336 1337 1337 1337 1313 1313 1314 1313 1314 1313 1305 1305 1305 200 200 200 200 200	Score
######################################	Query Match I
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CORE ANTIGEN. CHOLESTERYL ESTER TRAN CHOLESTERYL E	Description
9.32e-236 7.85e-231 2.85e-231 2.85e-231 7.06e-228 7.06e-228 7.06e-225 6.10e-224 9.24e-223 3.60e-222 5.66e-222 5.66e-222 5.66e-223 3.60e-223 3.60e-223 3.60e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-223 5.66e-	Pred. No.

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### ALIGNMENTS

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CORAL HPBYY STANDARD; PRT: 183 AA.  PO3146; 21-JUL-1986 (REL. 01. CREATED) 21-JUL-1986 (REL. 01. LAST EXQUENCE UPDATE) 21-JUL-1986 (REL. 01. LAST EXQUENCE UPDATE) 21-JUL-1986 (REL. 14. LAST ANNOTATION UPDATE) CORE ANTIGEN CORE	<b>L</b>

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01-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TONG S., LI J., VITVITSKI L., TREPO C.; "Active hepatitis B virus replication in associated with viral variants containing
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P24023;
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EMBL; A08967; G411874; -.
PIR; B93217; NKVLA2.
PFAM; PF00906; Hepatitis_cc
CORE PROTEIN; REPEAT.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 89010694.
OKAMOTO H., TSUDA F., SAKUGAWA H., SASTRO!
MIYAKAWA Y., MAYUMI M.;
MIYAKAWA Y., MAYUMI M.;
""""" hordiogy in
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21-JUL-1986
21-JUL-1986
01-OCT-1989
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01-AUG-1990
01-FEB-1991
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PASEK M., GOTO T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                    CORE ANTIGEN
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                                                                                                                                                                                HEPATITIS
                                                                                                                                                                                                                                                                                      P17392;
                                                                                                                                                                                                                                                                                                               CORA_HPBVO
                                                                                                                                                            VIRUSES;
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l Similarity 96.7%;
177; Conservative
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170
183 AA;
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(REL.
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                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                         O VIRUSES; H
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177
21042 MW;
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LAST SEQUENCE UI
LAST ANNOTATION
                                                                                                                                                         E ADW / STRAIN OKINAWA/PODW282)
HEPADNAVIRIDAE; ORTHOHEPADNAVI
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ANNOTATION UPDAT
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Pred. No. 7.85e-231;
5; Mismatches 1;
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                                                                       SASTROSOEWIGNJO R.I.,
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                                                                                                                                                            ORTHOHEPADNAVIRUS.
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Best Local
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P03150; P03151;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
01-FEB-1991 (REL. )
MEDLINE: 89010694.
OKAMOTO H., TSUDA F.,
MIYAKAWA Y., MAYUMI M
                                                                                                                                                                               ONO Y., ONDA H., SASADA R., IGARASHI K., 9
"The complete nucleotide sequences of the DNA; subtype adr and adw.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM;
CORE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                        MATSUBARA K.;
"Cloning and
                                                                                                             MEDLINE: 83246570.
FUJIYAMA A., MIYANOHARA
                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                          HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADR4), AND HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN INDONESIA/PIDW420). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                      STRAIN-ADR4
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                       NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D00330; -; NOT_ANNOTATED_CDS
                                               SEQUENCE FROM
                                                                     NUCLEIC
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                    ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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170
183 AA;
                                                                                        structural analyses of hepatitis
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                                               N.A.
                                                                                                                                                                       RES.
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17,
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96.2%;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
              SAKUGAWA
                                                                                                               Α.,
                                                                                                              NOZAKI C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1336; DB 1;
Pred. No. 2.85e-228;
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            Η.,
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              SASTROSOEWIGNJO
                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                              YONEYAMA T.,
                                                                                                                                                                                           SUGINO Y
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                                                                                                                                                                                           Y., NISHIOKA K.;
d hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 183;
                                                                                         virus
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            R.I.,
                                                                                                               OHTOMO N.,
                                                                                         DNAs, subtype
              IMAI
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01-AUG-1990
01-FEB-1991
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; V00867; -; NOT_ANNOTATED_CDS.
EMBL; X01587; G59407; -.
EMBL; D00331; -; NOT_ANNOTATED_CDS.
PIR; A93480; NKVLA5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; D00329; -; NOT_ANNOTATED_CDS PIR; A28925; NKVLJ1.
                                                                                                                                                      comparison of surface antigen subtypes.
J. GEN. VIROL. 69:2575-2583(1988).
                                                                                                                                                                                                          MEDLINE: 89010694.
OKAMOTO H., TSUDA F.,
                                                                                                                                                                                                                                                                                    CORE ANTIGEN.
HEPATITIS B VIRUS
                                                                                                                                                                                                                                                                                                                                                        CORA_HPBVJ
P17391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PFAM; PF00906; Hepatitis_core;
CORE PROTEIN; REPEAT.
                                                                                                                                                                                 "Typing hepatitis B virus by homology in nucleotide sequence:
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        VIRUSES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nparison of surface antigen subtypes."; GEN. VIROL. 69:2575-2583(1988).
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: B93460; NKVLA4.
: C28925; NKVLJ3.
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l Similarity 95.6%;
175; Conservative
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183 AA;
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(REL. 15,
(REL. 17,
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LAST
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                                                                                                                                                                                                                                                                        HEPADNAVIRIDAE;
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ANNOTATION UPDATE)
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Best Local S
Matches 17
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21-JUL-1986
01-OCT-1989
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REPEAT
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"The complete nucleotide sequences of the
DNA; subtype adr and adw.";
NUCLEIC ACIDS RES. 11:1747-1757(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 83168919. ONO Y., ONDA H., S
                                                                                                                                                                                                                                                                                                                 PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00906; Hepat:
CORE PROTEIN; REPEAT
                                                                                                                                                                                                                                                                                                                                                                            EMBL; V00866; -;
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    CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
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                                                                                                                                                                 ch 63.3%;
l Similarity 96.2%;
178; Conservative
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176; Conser
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larity 96.2%;
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HEPADNAVIRIDAE;
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ANNOTATION UPDATE)
                                                                                                                                                                 Score 1321; DB 1;
Pred. No. 2.56e-225;
4; Mismatches 1;
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Pred. No. 1.62e-225;
3; Mismatches 4;
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d hepatitis B
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CORE ANTIGEN.
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P29178;
                          "Identification of a new hepatitis that expresses HBV surface antigen {\tt J}. GEN. VIROL. 74:1627-1632(1993).
                                                                                                                           MEDLINE; 93346970.
NAUMANN H., SCHAEFER
GERLICH W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 90169850.

BHAT R.A., ULRICH P.P., VYAS G.N.;

"Molecular characterization of a new variant a persistently infected homosexual man.";

HEPATOLOGY 11:271-276(1990).
                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 93346970.
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VIRUSES; RETROID V
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173; Conser
                                                                                                                                                                                                                                                                                            S B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).
RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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195 AA;
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(REL. 24, LAST SEQUENCE UPDATE)
(REL. 24, LAST ANNOTATION UPDATE)
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(REL. 32, LAST SEQ
(REL. 32, LAST ANN
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                                    HBV surface antigen 74:1627-1632(1993).
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22461 MW;
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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ANNOTATION UPDATE)
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Pred. No. 6.10e-224;
9; Mismatches 3;
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subtype
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                                                                                                                                                                GASPAR A.M.C., REPP
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                                                                  (HBV) genotype adw4.";
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Best Local
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01-OCT-1989 (
01-OCT-1989 (
01-APR-1990 (
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial continues a linear property (Soc. http://creativecommercial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       "The complete nucleotide sequence of the genome of a hepatitis virus isolated from a naturally infected chimpanzee."; J.\ \text{GEN}.\ \text{VIROL}.\ 69:1383-1389(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X69798; G59423; -. PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                     PIR; A28885; NKVLCP
                                                                                   EMBL; D00220; D1000603; -.
                                                                                                                                                                                                                                                                             VAUDIN M., WOLSTENHOLME A.J., TSIQUAYE K.N., ZUCKERMAN A.J
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   HEPATITIS B VIRUS
VIRUSES; RETROID V
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171; Conser
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(REL. 12, LAST SEQUENCE UPDATE)
(REL. 14, LAST ANNOTATION UPDATE)
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llarity 92.9%;
Conservative
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203 5
188 1
195 2
203 3
24234 MW;
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    WW.
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Pred. No. 9.59e-224;
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3 X 5 AA REPEATS
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    1AFF57C9 CRC32;
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Best Local :
                   CORA_HPBV9
P17099;
01-AUG-1990 (
01-AUG-1990 (
01-AUG-1992 (
CORE ANTIGEN:
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(IN) FIELD B.N., JAENISCH R., FOX C.F. (EDS.);
ANIMAL VIRUS GENETICS, PP.57-70, ACADEMIC PRESS,
PIR; A94409; NKVLA3.
PFAM; PF00906; Hepatitis_core; 1.
CORE PROTEIN; REPEAT
172
179
REPEAT
172
179
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01-AUG-1992
15-DEC-1998
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P03148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 62.5%;
1 Similarity 95.7%;
177; Conservative
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173; Conser
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(REL.
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                                                                                                                               STANDARD;
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                                         15, CREATED)
15, LAST SEQUENCE UPDATE)
23, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01, CREATED)
23, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
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94.5%;
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1305; DB 1;
Pred. No. 3.60e-222;
4; Mismatches 2;
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Pred. No. 9.24e-223;
6; Mismatches 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 185;
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Best Local S
Matches 17
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WOODCHUCK HEPATITIS VIRUS 7
WOODCHUCK HEPATITIS VIRUS 5
WOODCHUCK HEPATITIS VIRUS 8
VIRUSES; RETROID VIRUSES; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORA_WHV1 STAN
P031S2;
21-JUL-1986 (REL. C
21-JUL-1986 (REL. C
21-JUL-1986 (REL. C
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VIRUSES; R
                                                                                                  SPECIES-WOODCHUCK HEPATITIS MEDLINE; 88101359.
COHEN J.I., MILLER R.H., ROS
                                                                                                                                                                                                                                                              "Nucleotide sequence of a cloned woodchuck hepatitis virus comparison with the hepatitis B virus sequence.";
J. VIROL. 41:51-65(1982).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SPECIES-WOODCHUCK HEPATITIS
MEDLINE; 82216969.
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             GALIBERT F., CHEN T.N.,
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                                          'Sequence comparison of woodchuck hepatitis
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conservation of the genome
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177; Conser
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G
                                                                              R.H.;
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RETROID V
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B-1990) TO EMBL/GENBANK/DDBJ
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01, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
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95.2%;
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                                                                                                                                                                                                                                                                                                                                                                    MANDART E.;
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JS 7 (WHV 7),

JS 59 (WHV 59), AND

JS 8 (INFECTIOUS CLONE) (

JS 8 (INFECTIOUS CLONE) (
                                                                                                        ROSENBLUM
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HEPADNAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1304; DB 1;
Pred. No. 5.66e-222;
5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                               VIRUS 1;
                                                                                                                                                                         VIRUS
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                                                                                                                                                                         7,
                                                                                                     B.,
                                                                                                                                                                         AND
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Best Local Similarity
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EMBL; M18752; G336140; -.
EMBL; M19183; G336145; -.
EMBL; J04514; G336149; -.
PIR; A03713; NKVLCT.
PIR; C32397; NKVLCT.
PIR; C32397; NKVLC4.
PIR; C32397; NKVLC4.
PIR; C32397; NKVLC4.
                                                                                                                                                                                                                                                                                            CORA_WHV8
P06433;
01-JAN-1988
01-JAN-1988
01-OCT-1989
                                   KODAMA K., OGASAWARA N., Yu
"Nucleotide sequence of a evolutional relationship by VIROL. 56:978-986(1985)
                                                                                                             MEDLINE; 86
KODAMA K.,
                                                                                                                                                                                                       WOODCHUCK HEPATITIS VIRUS 8 (WHV 8).
VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE;
                                                                                                                                                                                                                                                                              CORE
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GIRONES R., COTE P.J.,
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[3]
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                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 86062931.
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larity 67.08;
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25; Mismatches 32;
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hepadnaviruses.";
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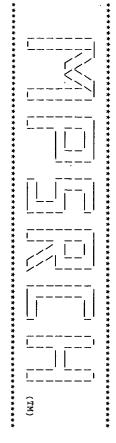
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Query Match 44.7%;
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Matches 128; Conservative
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                                                                                                   REPEAT
SEQUENCE
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PIR: A03715; NKVLS.
PFAM: PF00906; Hepatitis_core;
CORE PROTEIN; REPEAT.
REPEAT 196 203
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEEGER C., GANEM D., VARMUS H.E.;
"Nucleotide sequence of an infectious molecularly cloned genome ground squirrel hepatitis virus.";
J. VIROL. 51:367-375(1984).
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VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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25189 MW;
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Pred. No. 1.83e-149;
26; Mismatches 33;
Score 934; DB 1; L
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22; Mismatches 32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:26:11 1999; MasPar time 19.81 Seconds 765.940 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US3869-29-38183 (1-278) from us3869-29-38183.pep

Scoring table: PAM 150 Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl9

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.475; Variance 103.566; scale 0.449

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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#### ALIGNMENTS

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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA I
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. No. 3.17e-226;
Mismatches 0;
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. No. 7.57e-226;
Mismatches 0;
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HEPATITIS B VIRUS.
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E
EMBL; X85284; G736098; -.
EPRAM; PF00906; Hepatitis_core; 1.
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LUAM M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI SUBM MITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA I EMBL; X85291; G736119; -.
PFAM; PF00906; Hepatitis core; 1.
SEQUENCE 212 AA; 24336 MW; E0E4C243 CRC32;
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182; Conser
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RETROID VIRUSES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL.
(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06; Hepatitis_core;
183 AA; 21102 MW;
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(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDAT
C GENES (FERRACUTI 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.8%;
llarity 99.5%;
Conservative
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larity 98.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEPADNAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1373;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                Score 1374; DB 14;
Pred. No. 4.90e-226;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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7.57e-226;
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Matches 18
                                                                                                          01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
PRE C/C ORF.
HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES; H
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Q89597;
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01-NOV-1996
                                                                                              VIRUSES;
SEQUENCE FROM N.A.
STRAIN-PATIENT CI, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (SEP-1995) TO EMBL/GIEMBL; X72702; G288930; --
EMBL; X72702; G288930; --
EMBL; X80925; E198084; --
PFAM; PF00906; Hepatitis_core;
SEQUENCE 212 AA; 24336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SUB-TYPE AYW;
MEDLINE; 94079539.
PREISLER-ADAMS S., SCHLAYER M.J.,
RASENACK J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KARAYIANNIS
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VIRUSES; RETROID '
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larity 98.9%;
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                                                                                                                      HEPADNAVIRIDAE;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1374; DB 14;
Pred. No. 4.90e-226;
2; Mismatches 0;
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                                                      Q68066;
Q68066;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
X, PREC AND
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RAO B.S., CASEY J.L., RINAUDO J.S., KORBA
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ
EMBL; U95551; G2182120; -.

PFAM; PF00906; Hepatitis_core; 1.

SEQUENCE 212 AA; 24360 MW; 73AC92DB CF
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EMBL: X65258; G59466; -.
PFAM; PF00906; Hepatitis_core;
SEQUENCE 212 AA; 24348 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESQC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182;
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1 Similarity 98.9%;
182; Conservative
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Similarity 98.9%;
182; Conservative
                                                                                                                                                                                                                                                                                                                                                    278
                                                              (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
C GENES (LICHERI 2).
                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1372; DB 14;
Pred. No. 1 17e-225;
Pred. Wiematches 0;
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Pred. No. 7.57e-226;
2; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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HEPATITIS B

VIRUS

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STRAIN-PATIENT LICHERI-2'87;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITIED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X85314; G736204; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 183 AA; 21102 MW; 6F38AA3B CRC32;

VIRUSES;

RETROID

VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS

SEQUENCE FROM N.A.

Query Match 65.6%; Score 1370; DB 14; Best Local Similarity 98.4%; Pred. No. 2.78e-225; Matches 180; Conservative 3; Mismatches 0;

Length 183; Indels

0;

Gaps

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SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRTPRRRTPSPRRRRSQSPRRRRSQSRE 180

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MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL 155

CWGDLMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV 120 CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV

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RESULT 10
ID Q68025
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Best Local S
Matches 18
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Q68068;
Q1-NOV-1996
Q1-NOV-1998
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STRAIN-PATIENT LICHERI-3'90;
LAI M.E., MAZZOLENI A.P., PORRU A., BALEST
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ
EMBL; X85315; G736207; -.
EMBL; X85315; G736207; -.
SEQUENCE 212 AA; 24366 MW; AB227A9B CF
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                                                                                                                                                                                                                                                                                                                                        182; Conservative
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RETROID VIRUSES; HEPADNAVIRIDAE;
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G (TREMBLREL.
     PRELIMINARY;
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Pred. No. 2.78e-225;
1; Mismatches 1:
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
     PRT;
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AB227A9B CRC32;
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     212 AA
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Best Local S
Matches 18
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Q67872;
Q67872;
O1-NOV-1996
O1-NOV-1996
O1-NOV-1998
PRE C/C ORF.
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PRE-C/CORE.
HEPATITIS B
VIRUSES; RE
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01-NOV-1996
01-NOV-1996
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LIAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., I
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X65257; G59431; -
PFAM; PF00906; Hepatitis core; 1.
SEQUENCE 212 AA; 24348 MW; A6BD9DA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85293; G736126; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRUSES; RETROID VIRUSES;
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STRAIN=PATIENT CASTAG'3;
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Local Similarity 98.4%;
les 181; Conservative
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ESQC
                                                       GMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYRDALESPEHCSPHHTALRQAI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESQC
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Pred. No. 2.78e-225;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1369; DB 14;
Pred. No. 4.30e-225;
2; Mismatches 1;
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STRAIN-PATIENT VITTORINA'92;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E
EMBL; X85256; G736052; -.

PFAM; PF00906; Hepatitis_core; 1.

SEQUENCE 212 AA; 24322 MW; 83D9780B CRC32;
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M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMINITED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANK
EMBL; X85296; G7363139; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24308 MW; 69D87B53 CRC32;
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HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
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Pred. No. 4.30e-225;
3; Mismatches 0;
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01-NOV-1998
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HEPATITIS B VIRUSES;
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Q68010;
                                                                                     STRAIN-PATIENT GIORDO'84;
LIAM M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85316; G736210; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24376 MW; 80F52D0F CRC32;
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LIAI M.E., MAZZOLENI A.F., PORRU A., BALESTRIERI A.;
SUBAI M.E. (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85285; G736100; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24292 MW; 04A4D12D CRC32;
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Pred. No. 6.64e-225;
2; Mismatches 1;
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Search completed: Thu Dec 16 13:27:58 1999 Job time: 107 secs.

US3890-10-38183

MOIDPYREFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGELMTLAT WIDDYREFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHTEAT WYGVNLEDPASRDLVVSYVNLLLQMDFGFPEHLLVDFLQSLSMDIDPYREFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGELMTLATWYGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLVSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSOSRESQC1

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Thu Dec 16 13:44:26 1999; MasPar time 13.43 Seconds 467.254 Million cell updates/sec

Description: Perfect Score: Title:

Sequence: >US3890-10-38183 (1-295) from us3890-10-38183.pep 2205 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 295

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 23:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 33.363; Variance 173.459; scale 0.192

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DВ	ID	Description	Pred. No
1	1375	62.4	194	32	W50242	Hepatitis B virus pre	1.29e-99
2	1375	62.4	212	ω 2	W50250	B virus	9
w	1375	62.4	346	ഗ	R27473	О.	1.29e-99
4	1363	61.8	184	دسو	P80959		1.24e-98
տ	1358	61.6	183	32	W50251	B virus	3.17e-98
σ	1359	61.6	193	32	W50241	B virus	2.63e-98
7	1353	61.4	183	20	W09044	itis B virus	8.14e-98
œ	1349	61.2	183	_	R05635	Hepatitis B antigen.	1.73e-97
φ	1349	61.2	183	ஶ	P00041		1.73e-97
10	1344	61.0	397	20	W09048	Plasmid pHBV DN AA en	4.43e-97
11	1338	60.7	184	G	P00004	Sequence of core anti	1.37e-96
12	1336	60.6	196	80	R40806	Hepatitis B core / PV	2.00e-96
13	1337	60.6	208	8	R40808		
14	1334	60.5	183	4	P40311	Hepatitis virus core	
15	1334	60.5	183	ω	R40805	Hepatitis B core prot	
16	1334	60.5	183	<u>.</u>	R68868	IJ	2.91e-96

45	44	43	42	41	40	39	38	37	3 6	<u>3</u> 5	3 4	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18
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# ALIGNMENTS

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                                                                                                                                                                                                                         PT DNA encoding proteins which can be incorporated with wild type protein shibition of viral replication, especially hepatitis B virus PT inhibition of viral replication, especially hepatitis B virus PS Claim 15; Page 35; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25) PS Claim 15; Page 35; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25) Protein that is encoded by the full-length HBV precore gene. Evidence is provided that HBV replication is inhibited in the protein scan be incorporated into HBV nucleocapsids along vith the p21 core protein see W50251), which is the usual nucleocapsid component, and thereby render the nucleocapsids deficient in encapsidating HBV pregenomic RNA. Thus, overexpression of the precore proteins, or certain variants of them, cleads to transdominant inhibition of HBV replication. Suitable inhibitory proteins include p25, p22 (see W50241), Met-p22 (see W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18 (Het (see W50238)). The inhibitory proteins can be produced by recombinant methods using claimed expression vectors and host cells. They can be provided exogenously to the target cells for construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.
                                                                                        Matches
                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatocyte; liver; person hepatitis B virus. W09809649-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the target cells for use in inhibiting HBV replication. Alternatively, a nucleic acid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.

Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1998 (first entry)
Hepatitis B virus precore p25 polypeptide.
Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1997; U15500.
03-SEP-1996; US-023370.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, Wands JR;
WPI; 98-193325/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W50250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ת 2
W50250 standard; Protein; 212 AA.
                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71
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gmdidpykefgatvellsflpsdffpsvrdlldtasalyrealespehcsphhtalrqai 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   esqc 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183;
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                                                                                                                                                                                                            212
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                                                                                        Conservative
                                                                                                                                                                                                            ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p25 protein.
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99.5%;
                                                                                                                 62.4%;
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Pred. No. 1.
1; Mismatc
                                                                                 Score 1375; DB 32;
Pred. No. 1.29e-99;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                             Length 212;
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SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 171

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163 nmdidpykefgatvellsflpsdffpsvrdlldtasalyrealespehcsphhtalrqai 222

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Gaps

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G
                                                                                              PT Vaccinating against viral infections such as rables, hepatitis B, PT Vaccinating against viral infections such as rables, hepatitis B, PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

CC The sequence given is encoded by an expression cassette which comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/CC core) which is precisely linked to the I3L promoter derived from CC vaccinia virus. This DNA sequence was linked to the S1 and S2 vaccinia virus. This DNA sequence was linked to the S1 and S2 recombinant expressing the HBV gene. Other HBV genes were also used in the construction of a NYVAC (Sepandam of the construction of the sequence was linked to the S1 and S2 vaccinia virus which has been modified by deletion of these gene CC vaccinia virus which has been modified by deletion of six non-essential regions of the genome encoding known or potential virulence factors. The deletion loci were engineered as recipient loci for the insertion of the three inserted sequences engineered inserted sequences ensured that any recombination that did occur would lead to disruption of the conscinia genome and would cause unviable vaccinia virus. See also
Query Match
Best Local Similarity
Matches 183; Consei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-1993 (firs
S12/core protein.
Hepatitis B virus;
vaccinia virus; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1992.
09-MAR-1992;
07-MAR-1991;
11-JUN-1991;
                                                                                    vaccinia ge
Q35501-864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VIRO-) VIRÓGENETICS CORP.

COX WI, De Taisne C, Francis J, Gettig RR, Johnson GP,
Limbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus S
Riviere M, Tartaglia J, Taylor J;

WPI: 92-331718/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-1991; US-666056.
11-JUN-1991; US-713967.
06-MAR-1992; US-847951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg; vaccinia virus; 13L; promoter; NYVAC; recombinant; HBV L; vaccinia virus; 13L; promoter; NYVAC; recombinant; S12/core; large pre-S antigen; lasAg; fusion protein; pre-S region; S12/core; S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q29105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region
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                                                                     346 AA;
62.4%;
larity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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109..163
/label S2
164..346
/label Cor
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 Score
Pred.
1; M
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 re 1375; DB 5; L
d. No. 1.29e-99;
Mismatches 0;
                                  Length 346;
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pp 07-DEC-1987; 310725.

pp 07-DEC-1987; US-106538.

pr 07-OCT-1987; US-106538.

pr 07-OCT-1987; US-939617.

pr 07-OCT-1987; US-939617.

pr 07-OCT-1987; US-939617.

pr 107-OCT-1987; US-939617.

pr 108-163287/24.

pr 108-1632
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Best Local S
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   W50251 standard;
W50251;
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EP-271302-A.
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Conjugate; fusion protein; hepatitis B core protein; HBV subtype ayw.;
T cell stimulating polypeptide; vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subjects
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P80959 standard; protein; 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also P80896-P80898 and
                                                                                                                                                                                                                                esqc 184
                                                                                                                                                                                                                                                                                                                                         vsfgvwirtppayrppnapilstlpettvvrrrgrsprrrtpsprrrrsgsprrrrsgsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                               CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTF-GRETVIEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL 172
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183; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%;
llarity 99.5%;
Conservative
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                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P80951-P80859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1363; DB 1;
Pred. No. 1.24e-98;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               indels 1;
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RESULTING ACCORDANCE OF THE CONTROL OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT DNA encoding proteins which can be incorporated with wild type routeloospsid subunit(s) into a viral nucleocapsid - useful for proteins which replication, especially hepatitis B virus plsclosure; Page 41-42; 60pp; English.

CC This is the 21 kDa (p21) protein of hepatitis B virus (HBV) that cassembled into a 180 kSa subunit nucleocapsid structure that promotes viral replication. Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV replication is inhibited in the presence of high levels of HBV replication into HBV nucleocapsids along with the p21 core protein and thereby render the nucleocapsids along with the p21 core protein card thereby render the nucleocapsids deficient in encapsidating HBV regenemic RNA. Thus, over-expression of the precore protein or certain variants of them, leads to transdominant inhibition of HBV replication. Suitable inhibitory proteins include p25 (see w50250), p22 (see w50231) and wet-p12 (see w50242), p18 (see w50235), wet-p18 (see w50237) and wet-p18-het (see w50232). These proteins can be produced by recombinant methods using claimed expression construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.

Converse of the produced by recombinant methods using claimed expression of cells cacid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.
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Best Local
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12-MAR-1998.
03-SEP-1997; U15500.
03-SEP-1996; US-025370.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP, Wawpi; 98-193325/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1998 (first entry)
Hepatitis B virus p21 core protein.
Viral replication, inhibitor; HBV; nu
hepatocyte; liver; p21; core protein.
Hepatitis B virus.
                                                                                                          Hepatitis B virus precore p22 polypeptide. Viral replication; inhibitor; HBV; nucleocapsid; hepatocyte; liver; p22 protein.
 W09809649-A1
12-MAR-1998.
                                                                                                                                                                    W50241;
28-SEP-1998
                                                                                                                                                                                                         W50241 standard; Protein;
                                                        Region
                                                                         Key
                                                                                           Hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                     CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
181; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                             virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.6%;
larity 98.9%;
Conservative
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                     ocation/Qualifiers
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                                                                                                                                                                                                           193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1358; DB 32;
Pred. No. 3.17e-98;
1; Mismatches 1;
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                                                                                                                                gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT DNA encoding proteins which can be incorporated with wild type protein proteins which a viral nucleocapsid - useful for nucleocapsid subunit(s) into a viral nucleocapsid - useful for protein that is produced by elimination of the 19-amino acid leader CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22) CC protein that is produced by elimination of the 19-amino acid leader CC w50250). Evidence is provided that HBV precore protein (see CC w50250). Evidence is provided that HBV replication is inhibited in CC the presence of high levels of HBV precore or precore-related CC proteins. These proteins can be incorporated into HBV nucleocapsids CC along with the p21 core protein (see w50251), which is the usual CC uncleocapsid component, and thereby render the nucleocapsids CC deficient in encapsidating HBV pregenomic RNA. Thus, over-cxpression of the precore proteins, or certain variants of them, CC leads to transdominant inhibition of HBV replication. Suitable CC inhibitory proteins include p25 (see w50250), p22, Met-p22 (see W50242), p18 (see w50236), Met-p18 (see W50237) and Met-p21 (see W50244-49) may be consisted into the p22 and Met-p22 (see W50244-49) may be consisted into the p22 and Met-p22 (see W50244-49) may be consisted into the p22 and Met-p22 (see W50244-49) may be consisted into the p25 or use in inhibiting HBV replication. CC Alternatively, a nucleic acid construct that directs overexpression cc therapy of HBV infection.

Sequence 193 AA:
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Best Local
                misc_difference
                                                                                misc_difference
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03-SEP-1996; US-025370.
(GEHO ) GEN HOSBITAL CORP.
Melegari M. Scaglioni PP, Wands
WPI; 98-193325/17.
                                                                                                                                                                                                                 ground
                                                                                                                                                                                                                                                            W09044 standard; Protein; 183
W09044;
11-APR-1997 (first entry)
                                                                                                                                                                                                 core
                                                                                                                                                                                                            Hepatitis B virus core protein.
Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus; ground squirrel hepatitis B virus; duck hepatitis B virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                               Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                             232
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                                                                                                                                                  isc_difference 71..180
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                                                                                                                                                                                                                                                                                                                                                                                                                         gmdidpykefgatvellsflpsdffpsvrdlldtasalyrealespehcsphhtalrqai 69
                                                                                                                                                                                              protein; replication; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.6%;
larity 98.4%;
Conservative
               polypeptides of 171..180
                                                                                polypeptides of 81..180
                                             /note= "C-terminus of core protein is at a acid position between 81 and 180 in mutant
                                                                                                             /note= "C-terminus of core protein is at any acid position between 71-180 in mutant
                                                                /note= "C-terminus of
                                                                                                                                                                ocation/Qualifiers
 "C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1359; DB 32; Pred. No. 2.63e-98; 2; Mismatches 1;
                                the
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                                                                                              the invention
 o
f
                              invention
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protein is
                              (Claim
                                                                                            (Claim 23)"
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Best Local
Synthetic.
EP-374869-A.
27-JUN-1990.
                                   Hepatitis B antigen
Hepatitis B virus;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 55-56; 83pp; English.
Alteration of the C-terminus of the core protein (W09044) of hepatitis B virus (HBV) or other hepadnavirus creates a mutant polypeptide capable of reducing replication of the wild-type virus by a dominant negative mechanism. The inhibitory effect is species-specific and is achieved by deletion of a few C-terminal amino acids from the core protein, and/or by joining the core protein to a hepadnavirus surface protein (see also W09045), creating a core-surface fusion. Such mutant polypeptides (see also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
                                                            R05635 standard; protein; 183
R05635;
30-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method for inhibiting the replication of hepadnaviruses comprises introducing a mutant polypeptide with a mutated core protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-1995; US-017814.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
WPI; 97-087176/08.
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-1997.
20-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9700698-A1.
                                                                                                                                           293
                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                             infection.
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                                                                                                                                                                                                                                                                                             mdidpykefgatvellsflpsdffpsvrdlldtasalyrealespehcsphhtalrqail 60
                                                                                                                                                                  sqc
                                                                                                                                                                                                      sfgvwirtppayrppnapilstlpettvvrrpgrsprrrtpsprrrrsgsprrrrsgsre 180
                                                                                                                                                                                                                                          SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRE
                                                                                                                                                                                                                                                                                                                                              l Similarity
181; Conser
                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                                               183 AA;
                                                  antigen.
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "C-terminus of c
position 178 in mutant
invention (Claim 7)"
172.183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminus of core protein is acid position between 174 and 180 in polypeptides of the invention (Claim 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides
174..180
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position 178 in mutant
invention (Claim 7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are deleted from the core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid position between 171 polypeptides of the invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "amino acid residues 172-183,
                                                                                                                                                                                                                                                                                                                                                         61.4%;
                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wands
                                      HBV;
                                                                                                                                                                                                                                                                                                                                                         Score 1353; DB 20; Pred. No. 8.14e-98;
                                      ds
                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Length 183;
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of the
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6)"
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f the
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R (01-NOV-1377).

R (BIOJ) Biogen Inc.

A (BIOJ) Biogen Inc.

Parage K, Schaller HE;

DR WPI; 90-195067/26.

DR N-PSDB; Q04799

PT Recombinant DNA encoding Hepatitis B virus polypeptide antigens -

PT used in detection of infection and in vaccine prodn.

PS Disclosure; 4pp; English.

CC Polypeptide fragments encoded by the DNA sequence are antigenic for

CC Polypeptide fragments encoded by the DNA sequence may be used as a vaccine or in detection. Peptides may be

CC cultured in a suitable bacterial host such as E.coli.
                                                                                                   TRESULTION OF THE SULTION OF THE SUL
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Best Local S
Matches 17
  Query Match 61.2%;
Best Local Similarity 96.7%;
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1980.
21-DEC-1979; 303017.
22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
(BIOJ) BIOGEN NY.
MULTRY K, SCHALLER HE;
WPI; 80-57268C/33.
                                                                                           Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Example; Figs 3-4; 43pp; English.

Human serum from a single HBsAp positive, HBsAp positive donor (serotype adym) was used to prep. a DNA-contq. pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR32-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dG: TetR AmpS HBV+.
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22-DEC-1978; (
27-DEC-1978; (
01-NOV-1979; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of core antigen.
Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
Hepatitis B virus.
EP--1700-5
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8; GB-049907.
8; GB-050039.
9; GB-037910.
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Pred.
5; M
Score 1349; DB 5;
Pred. No. 1.73e-97;
5; Mismatches 1;
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No. 1.73e-97;
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Best Local S
Matches 17
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09-JAN-1997.
20-JUN-1995; U10602.
20-JUN-1995; US-017814.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
WPI; 97-087176/08.
                                                                                                                                                                                                                                                                                                                                                 Plasmid PHBV DN AA carries an insert (749598) coding for a prot (W09048) comprising a hepatitis B virus (HBV) core protein (see also W09045) at amino acid 179 with the HBV surf protein (see also W09045) at amino acid 8. Plasmid PHBV DN BB (749599) expresses the HBV core fused at amino acid 175 to the surface protein at amino acid 112 (W09049). HBV DN AA was at least as potent an inhibitor of HBV replication as construct PHBV DN (749597); PHBV DN BB was less inhibitory than PHBV DN. Vectors expressing hepadnavirus dominant negative core mutants be utilised in the gene therapy of viral infections.

Sequence 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB: T49598.

New method for inhibiting the replication of hepadnaviruses - comprises introducing a mutant polypeptide with a mutated core protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 46-48; 83pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
region
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W09048;
11-APR-1997 (first entry)
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                                                                              sfgvwlrtppayrppnapilstlpettvvrrrgrsprrrtpsprrrrsqsprrrrsqsre 180
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1 Similarity 100.0%;
179; Conservative
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/note= "positions 1-179 correspond to
1-179 of HBV core protein"
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180..397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "positions 180-397 correspond
9-226 of HBV surface protein"
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Pred.
0; M
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                                                                                                                                                                                                                                                re 1344; DB 20;
1. No. 4.43e-97;
Mismatches 0;
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DN AA.
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Best Local
                                                                                                                                                                                                       Hepatitis B core / PV-
Hepatitis B; core; HBC
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1980.
21-DEC-1979; 303017.
22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
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                                                                                                                                                                                                                                                                                                              R40806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Claim 13; Page 40; 43pp; English.

Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contg. pellet which was labelled with 3H or 32p as described by p. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR32-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dG: HBV-KPN I dC: Tetk AmpS HBV+.
J05192170-A.
03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus; antigen; antibody; diagnosis; vaccine Hepatitis B virus. Ep--13828-A.
                                                                                                                                    protein
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Murray K, Schaller HE;
WPI; 80-57268C/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
                                                                                                                                                                                                                                                                                                                                     standard;
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177; Conser
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14..196
/label=
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     Protein;
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PV-1 fusion
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Pred. No. 1.37e-96;
5; Mismatches 1
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R40808;
R40808;
16-FEB-1994
                                                                                                                                                                                                                                                                                                             Disclosure; Fig 9, 12pp; Japanese.

The hepatitis B core gene is recombined with PV-1 DN and IL-1 beta to form a plasmid (Q47738) which is the a vaccine. NB: Sequence is difficult to read in the
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The hepatitis B core gene is recombined with PV-1 DNA and IL-1 beta to form a plasmid (Q47738) which is then used a vaccine. NB: Sequence is difficult to read in the original
                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant plasmid for high immunogenity recombined haemagglutinin gene, hepatitis virus and exotic genes
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24-SEP-1991; 243800.
24-SEP-1991; JP-243800
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N-PSDB; Q47736.
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26..208
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HBC;
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PV-1; IL-1 beta;
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                                                                                                                         Score 1337; DB 8; Pred. No. 1.66e-96; 7; Mismatches 3;
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Best Local S
Matches 17
                                                                    Hepatitis B core protein.
Hepatitis B; core; HBC; PV-1
Hepatitis B Virus.
J05192170-A.
J05192170-A.
J3-AUG-1993; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS L.
WPI; 93-277479/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA used in prevention of infections by hepatitis virus B - comprises structural gene of hepatitis virus adr B surface antigen coding gene and at least 1 virus core antigen structural gene. Disclosure: Fig 3; 13pp; Japanese.

The sequence is that of hepatitis virus core antigen (HBcAg). It can be used as a vaccine for the prevention of infections by hepatitis B virus (HBV) and also in the diagnosis of early stages of HBV infection. See also p40310.

Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-1984.
19-0CT-1982; JP-183432.
19-0CT-1982; JP-183432.
19-0CT-1982; JP-183432.
(TAKE) TAKEDA CHEMICAL IND
WPI; 84-143231/23.
Recombinant plasmid for high immunogenity recombined haemagglutinin gene, hepatitis virus and exotic genes
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R40805 standard; Protein; 1
R40805;
16-FEB-1994 (first entry)
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HBCAG; vaccine; diagnosis; HB
Hepatitis b virus.
J59074985-A.
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Local Similarity 95.6%;
hes 175; Conservative
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                                                                                                                                                                                                                                                                  PV-1; IL-1 beta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1334; DB 4; I
Pred. No. 2.91e-96;
5; Mismatches 3;
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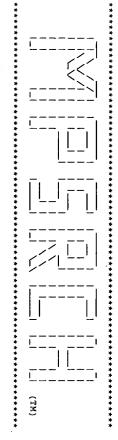
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Best Local Similarity 95.6%;
Matches 175; Conservative
                                                                                                                                                                                                            Disclosure: Fig 6; 12pp; Japanese.

The hepatitis B core gene is recombined with PV-1 DNA and II-1 beta to form a plasmid (Q47738) which is then used to a vaccine. NB: Sequence is difficult to read in the original specification.

Sequence 183 AA;
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 293
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                                         SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSRE
                    183
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Pred. No. 2.91e-96;
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Search completed: Thu Dec 16 13:47:38 1999 Job time: 192 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:47:54 1999; MasPar time 14.55 Seconds 812.638 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

>US3890-10-38183 (1-295) from us3890-10-38183.pep 2205 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 295

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.101; Variance 117.991; scale 0.399

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

222223 222223 222223 22223 22223	Result
1373 1374 1374 1373 1370 1370 1360 1369 1369 1366 1366 1366 1366 1366 1366	Score
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60.6	60.7	60.7		60.8	60.8	60.8	60.8	60.9	60.9	61.0	61.0	61.1	61.1	61.2	61.2	61.3	61.3	61.5	61.5	61.5	
212	212	212	183	212	212	183	183	183	183	212	183	183	183	183	183	212	183	212	212	212	
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		ec.		e antigen precursor /	ecu	•	•	•	core antigen - hepati	ecu	•	•	,	•	core antigen - hepati	e antigen precursor /		e antigen precursor /			
2.04e-194	1.39e-194	9.43e-195	9.43e-195		4.36e-195	4.36e-195	4.36e-195	2.96e-195	2.01e-195	1.37e-195	9.31e-196	2.92e-196	2.92e-196	1.99e-196	1.99e-196	9.18e-197	9.18e-197	1.96e-197	1.96e-197	9.06e-198	

#### ALIGNMENTS

##residues 1-2 ##residues 53264 ##ccoss-references   ##ccoss-references   ##cccession S53264 ##molecule_type DNA ##residues 1-2: ##cross-references	##residues ##residues ##residues ##cross references ##cross references ##experimental_sour \$53209 ##molecule_type_DNA ##residues ##residues ##residues ##cross-references ##cross-references ##cross-references ##cross-references	##molecule_type DNA ##residues 1-2 ##cross-references: ##cross-references: ##experimental_sour REFERENCE S53112 #authors Lai, M.E #submission submittee #accession S53191	REFERENCE #authors #submission #description #accession	DATE ACCESSIONS	RESULT 1 ENTRY TITLE ALTERNATE_NAMES CONTAINS ORGANISM #variety
##molecule_type DNA ##residues   1-212 ##label LA3 ##coss-references EMBL:X85300; NID:g736150; PID:g736152 ##axperImental_source isolate patient Sanna'84 Cession S53264 cession B53264 ##molecule_type DNA ##residues 1-212 ##label LA4 ##residues 1-212 ##label LA4	##molecule_type DNA ##residues 1-212 ##label LAI ##cross-references EMBL:X85283; NID:g736088; PID:g736090 ##experimental_source isolate patient Ferracuti'83 cession 55309 ##molecule_type DNA ##residues 1-212 ##label LA2 ##cross-references EMBL:X85290; NID:g736114; PID:g736116 ##scross-references EMBL:X85290; NID:g736114; PID:g736116 ##scross-references EMBL:X85290; NID:g736114; PID:g736116	##molecule_type DNA ##rcsidues 1-212 ##label PLU ##rcss-references EMBL:Z35716; NID:g527435; PID:g527437 ##cross-references EMBL:Z35716; NID:g527435; PID:g527437 ##cross-references subtype ayw4, isolate hb321 NCE S53112 NCE S53112 Thors La1, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A. bmission submitted to the EMBL Data Library, March 1995 cession S53191	\$47404 Plucienniczak, A. Pluci	1solate patient Licheri'83 18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change 10-Oct-1997 \$47405; \$53191; \$53209; \$53234; \$53264; \$53249; \$53262; \$53277; A03711	NKVLAH #type complete e antigen precursor / core antigen - hepatitis B virus (subtype ayw4, isolate hb321 and others) HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen #formal_name hepatitis B virus, HBV subtype ayw4, isolate hb321; isolate patient Ferracuti'83; isolate patient Castag'83; isolate patient Sanna'84; isolate patient Licheri-1'85; isolate patient Fore-1'86;

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#title Nucleotide sequence of the ayw) in E. coli.
#cross-references MUID:81012091
#accession A03711
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##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
rcession $53277
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##experimental_source isolate patient Flore-1'86
scession $53262
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##cross-references GB:J02203; NID:g329640; PID:g329642
##experimental_source subtype ayw
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Similarity 99.5%;
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                                                                                                     HBc antigen
                                                                                                                     core antigen -
Castaa-2'87)
#formal_name hepatitis B virus, HBV
isolate patient Castaa-2'87
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galibert, F.; Mandart, E.;
                                                                                core antigen
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                                                                                                                                              #type complete
en - hepatitis
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                                                                                                                                          hepatitis
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Pred. No. 8.67e-201;
1; Mismatches 0;
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#submission
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                                                                                                                                                       ##experimental_source isolate patient Ferracuti-1'89
##note due to a stop codon between the alternative initiatiors
the e antigen precursor cannot be produced
                                                                                                                                                                                                                                                                       ##residues 1-212 ##label LAI
##cross-references EMBL:X85291; NID:g736117; PID:g736119
##experimental_source isolate patient Castag-1'85
cession S53197
                                                                                                                                                                                                                  ##residues 30-212 ##label LAW 30-212 ##cross-references EMBL:X85284; NID:g736095; PID:g736098
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##note due to a stop codon between the alternative
the e antigen precursor cannot be produced
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##experimental_source isolate patient Castaa-2'87
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##residues 30-:
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Similarity 99.5%;
182; Conservative
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submitted t
S53207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e antigen precursor / core antigen - hepatitis B (isolate patient Castag-1'85 and others)
HBc antigen; HBe antigen precursor / HBc antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          core antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate patient Castag-1'85; isolate patient Ferracuti-1'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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core protein
#length 183 #molecular-weight 21102 #checksum 2165
                                                                               #superfamily hepatitis B virus core antigen
alternative initiators; core protein
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#domain signal sequence #status predicted #label SIG\
#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
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to the EMBL Data Library, March 1995
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Pred. No. 1.88e-200;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                A.P.; Porru, A.; Balestrieri,
Data Library, March 1995
                                                                             core protein
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Matches 18
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Best Local
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30-178
179-212
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##cross-references EMBL:X72702; NID:g288927; PID:g288930
##experimental_source subtype ayw, patient C1000
##experimental_source subtype ayw, patient C1000
due to a stop codon between the alternative
the e antigen precursor cannot be produced
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                                                                  SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 171
                                                                                   GMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYRDALESPEHCSPHHTALRQAI
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   LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL
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1 Similarity 98.9%;
182; Conservation
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e antigen precursor / core antigen - he
(subtype ayw, patient C1000)
S HBe antigen precursor / HBc antigen; pr
core antigen; e antigen
#formal_name hepatitis B virus, HBV
subtype ayw, patient C1000
20-Feb-1995 #sequence_revision 20-Feb-1
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#superfamily hepatitis B virus core antigen
core protein
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submitted to the EMBL Data Library, March 1993
Identification and sequence analysis of hepatitis
in immunological negative infection.
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predicted #label ECP
#length 212 #molecular-weight 24336 #checksum 746
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

pth 212 #molecular-weight 24336 #checksum 770
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Pred. No. 1.28e-200;
2; Mismatches 0;
                                                                                                                                                Score 1374; DB 2;
Pred. No. 1.28e-200;
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##cross-references EMBL:X65258; NID:g59434; PID:g59436
##experimental_source subtype ayw, patient CI
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HBe antigen precursor / HBc antigen core antigen; e antigen

#formal_name hepatitis B virus, H

subtype ayw, patient CI

20-Feb-1955 #sequence_revision 20
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#formal_name hepatitis B virus, HBV isolate patient Licheri-2'87 08-Jul-1995 #sequence_revision 03-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, March
Sequence analysis of HBV genomes isolated
HBBAg negative chronic liver disease.
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e anti
                                                                             s53270 #type complete core antigen - hepatitis | Licheri-2'87)
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alternative initiators; core protein
                                                                HBc antigen
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                                                   core antigen
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recursor / core antigen - hepatitis B virus
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Pred. No. 1.88e-200;
2; Mismatches 0;
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                                                                                                 virus
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03-Aug-1995

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##cross-references EMBL:X85314; NID:q736201; PID:q736204
##experimental_source isolate patient Licheri-2'87
due to a stop codon between the alternative initiatiors
##note the e antigen precursor cannot be produced
                                                                                                                                                                                                                                              #experimental_source isolate patient Castag'3
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Ch 62.1%; Score 1370; DB 2; 1 Similarity 98.9%; Pred. No. 5.98e-200; 182; Conservative • 1; Mismatches 1;
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Similarity 98.4%;
180; Conservative
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Lai, M.E.; Maz
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S5311
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#formal_name hepatitis B virus, HBV
isolate patient Castag'3
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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HBe antigen precursor / HBc antigen;
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
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to the EMBL
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Pred. No. 5.98e-200;
3; Mismatches 0;
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Data Library, March 1995
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##cross-references EMBL:X85315; NID:g736205; PID:g736207
##experimental_source isolate patient Licheri-3'90
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Similarity 98.9%;
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e antigen precursor / core antigen - hepatitis
  (isolate patient Licheri-3'90)

S HBe antigen precursor / HBc antigen; pre-C/C accore antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate patient Licheri-3'90
08-Jul-1995 #sequence_revision 03-Aug-1995 #te
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Best Local Similarity 98.9%;
Matches 182; Conservative
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                                  ##residues 1-212 ##label LAI ##cross-references EMBL:X65257; NID:g59429; PID:g59431
                ##experimental_source subtype ayw,
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S53112
                                                                                                           submitted to the EMBL Data Library, March 1992
Sequence analysis of HBV genomes isolated from
HBSAy negative chronic liver disease.
                                                                                                                                                                                                                                                                 #formal_name hepatitis B virus,
subtype ayw, patient C
20-Feb-1995_#sequence_revision 2
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HBe antigen precursor / HBc antigen;
core antigen; e antigen
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#formal_name hepatitis B virus, HBV
isolate patient Vittorina'92
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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Pred. No. 8.80e-200;
1; Mismatches 1;
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HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen
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Pred. No. 8.80e-200;
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Pred. No. 8.80e-200;
3; Mismatches 0;
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(isolate pattent Chighine-1'85)
HBe antigen precursor / HBc antigen;
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(isolate patient Ferracuti-2'90)
HBe antigen precursor / HBc antigen;
                           core antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate patient Chighine 1'85
08-Jul-1995 #sequence_revision 03-Aug-1995
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to the EMBL Data Library, March 1995
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Pred. No. 1.30e-199;
2; Mismatches 1;
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##cross-references EMBL:X85316; NID:g736208; PID:g736210
##cross-references EMBL:X85316 patient gatient Glordo'84
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core antigen; e antigen
#formal_name hepatitis B virus,
isolate pattent Glordo'84
08-Jul-1995 #sequence_revision (
08-Sep-1997
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#length 212 #molecular-weight 24364 #checksum 1123
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Pred. No. 2.80e-199;
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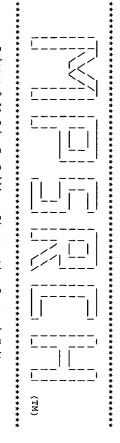
Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

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isolate patient Muresu'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:49:26 1999; MasPar time 10.05 Seconds 829.670 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US3890-10-38183 (1-295) from us3890-10-38183.pep 2205 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 295

Searched: PAM 150 Gap 11 77977 seqs, 28268293 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 48.376; Variance 105.353; scale 0.459

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4.00e-02 5.30e-02	2.27e-02 2.27e-02	1.71e-02	9.62e-03	9.62e-03	7.20e-03	7.20e-03	9.62e-03	4.02e-03	2.24e-03	2.24e-03	3.00e-03	3.00e-03	6.80e-04	5.04e-04	1.10e-04	2.58e-06	1.02e-07	3.71e-09

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Query Match 62.3%; Score 1374; DB 1; Length 183; Best Local Similarity 100.0%; Pred. No. 2.04e-230;	; V01460; G62278; ALT_INIT. ; X02496; -; NOT_ANNOTATED_CDS. A03711; NKVLAH. ; PF00906; HepatLt1s_core; 1. PROTEIN; REPEAT. AT 162 169 AT 170 177 AT 170 170 AT 170 170 AT 170 170 AT 170 170 AT 17	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	ENCE FROM N.A.  INE: 81012091.  BERT F., MANDART E., FITOUSSI F., TIOLLAIS P., CHAR  leotide sequence of the hepatitis B virus genome (s ed in E. coli.";  RE 281:646-650(1979).  ENCE FROM N.A. (CLONE PHB320).  INE: 85204397.  INE: 105: 208-212(1985).	CORA_HPBVY STANDARD; PRT; 183 AA.  P03146; P03146; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE) CORE ANTIGEN. C. HEPATITIS B VIRUS (SUBTYPE AYW). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

Matches

173

61

121

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Query Match
Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TONG S., LIJ., VITVITSKI L., TREPO C.;
"Active hepatitis B virus replication in 1
associated with viral variants containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M32138; G495034; ALT_SEQ. PIR; A34773; NKVLA1.
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TONG S. IT
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l Similarity 95.2%;
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21, LAST SEQUENCE UPDATE)
21, LAST ANNOTATION UPDAT
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Pred. No. 2.47e-227;
5; Mismatches 4;
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P03147;
21-JUL-1986
21-JUL-1986
01-OCT-1989
                                                                                                                                           CORA_HPBVO STANDARD; PRT; 183 AA.
p17392;
01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
CORE ANTIGEN.
HEPATITIS B VIRUS (SUBTYDE ADW / STRAIN OKINAWA/PODW282).
VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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REPEAT
SEQUENCE
SEQUENCE FROM N.A.

MEDLINE: 89010694.

OKAMOTO H., TSUDA F., SAKUGAWA H., SAST
MIYAKAWA Y., MAYUMI M.;

"Typing hepatitis B virus by homology i
comparison of surface antigen subtypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J02202; G329638; -.
EMBL; A08967; G411874; -.
PIR; B93217; NKVLA2.
PFAM; PF00906; Hepatitis_core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASEK M., GOTO T., GILBERT LEADBETTER G., MURRAY K.; "Hepatitis B virus genes ar NATURE 282:575-579(1979).
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VIRUSES; RETROID V
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183 AA;
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177
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12, LAST ANNOTATION
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Pred. No. 1.34e-225;
5; Mismatches 1;
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Best Local
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P03150; P03151;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
01-FEB-1991 (REL.)
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MEDLINE, 83168919.

ONO Y., ONDA H., SASADA R., IGARASHI K., S
"The complete nucleotide sequences of the
"The complete nucleotide sequences of the
DNA; subtype adr and adw.";

NUCLEIC ACIDS RES. 11:1747-1757(1983).
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MEDLINE: 89010694.
OKAMOTO H., TSUDA F., S
MIYAKAWA Y., MAYUMI M.;
                                             STRAIN=ADW;
MEDLINE; 89010694.
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SEQUENCE
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                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                  NUCLEIC
                                                                                                                                                                                             "Cloning
                                                                                                                                                                                                                         MATSUBARA K.;
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PF00906; Hepatitis_core;
PROTEIN; REPEAT.
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170
183 AA;
                                                                                                                                                                                             structural analyses of hepatitis
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01, LAST SEQUENCE UPDATE)
17, LAST ANNOTATION UPDATE)
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96.2%;
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                           SAKUGAWA
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Pred. No. 4.26e-223;
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                           SASTROSOEWIGNJO
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                                                                                                                                                                                                                                          YONEYAMA T.,
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P17391;
P17391;
O1-AUG-1990 (REL. 15, CREATEL)
O1-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
O1-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
CORE ANTIGEN.
HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN JAPAN/PJDW233).
HEPATITIS B VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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                                                                                                                                                                                                                                                                                       MEDLINE: 89010694.

ORAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO R.I., IMAI MIXARAWA Y., MAYUMI M.;

"Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes.";

J. GEN. VIROL. 69:2575-2583(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORA_HPBVJ
P17391;
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; D00329; -; PIR; A28925; NKV
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PIR; B93460; NKVLA4.
PIR; C28925; NKVLJ3.
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EMBL; X01587; G59407; -.
EMBL; D00331; -; NOT_ANNOTATED_CDS.
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GEN. VIROL. 69:2575-2583(1988).
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1 Similarity 95.6%;
175; Conservet
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177
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Pred. No. 1.03e-222;
5; Mismatches 3;
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PF00906;

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RESULT RESULT OF THE RESULT OF
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01-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CORE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORE PROTEIN; REPEAT REPEAT 162 1 REPEAT 170 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ONO Y., ONDA H., SASADA R., IGARASHI K
"The complete nucleotide sequences of one, subtype adr and adw.";
NUCLEIC ACIDS RES. 11:1747-1757(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 83168919
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                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; V00866; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                           173
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MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
                                                                                                                                                                                                                                                                                                                                               PROTEIN: REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                            C93460; NKVLA6
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                                                                                                            MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
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                                                                                                                                                                                               l Similarity
178; Conser
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176; Conser
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RETROID V
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172
185 AA;
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170
183 AA;
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(REL.
                                                                                                                                                                                          59.9%;
ilarity 96.2%;
Conservative
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                                                                                                                                                                                                                                                                                  171
179
; 21394 MW;
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01, LAST SEQUENCE UI
12, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
177
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96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E ADW).
HEPADNAVIRIDAE;
                                                                                                                                                                                             Score 1321; DB 1;
Pred. No. 3.29e-220;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1322; DB 1;
Pred. No. 2.11e-220;
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                                                                                                                                                                                                                                                                                    791E0381 CRC32;
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                                                                                                                                                                                                                                     Length 185
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d hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 183;
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RESULT 8
ID CARALPBUF
AC 29178;
DT 01-DEC-1992
DT 01-DEC-1992
DT 01-DEC-1992
DT 01-DEC-1992
DE CORE ANTIGEN
GN C.
OS HEPATITIS B V
OC VIRUSES; RETI
RN (1]
RP SEQUENCE FROM
RX MEDLINE; 9011
RP MEDLINE; 9017
RP MEDLINE; 917
RP ABHAT R.A., UI
RT "MOlecular cl
RT "MOlecular cl
RT a persistenti
RL HEPATOLOGY 11
DR PFAM; PF00900
FT REPEAT
SQ SEQUENCE 11
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Best Local S
Matches 17
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005495;

01-NOV-1995 (

01-NOV-1995 (

01-NOV-1995 (

CORE ANTIGEN.
                  "Identification of a new hepatitis that expresses HBV surface antigen J. GEN. VIROL. 74:1627-1632(1993).
                                                                                  MEDLINE; 93346970.
NAUMANN H., SCHAEFER
GERLICH W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE; 90169850.

BHAT R.A., ULRICH P.P., VYAS G.N.;

"Molecular characterization of a ne
a persistently infected homosexual

HEPATOLOGY 11:271-276(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A37182; NKVLH3. PFAM; PF00906; Hepat CORE PROTEIN; REPEAT
                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 93346970.
                                                                                                                                                                                                                      HEPATITIS
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                                                                                                                                                                                             VIRUSES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 AA;
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(REL.
                                                                                                                                                                                                                                                                                    (REL. 32, CREATED)
(REL. 32, LAST SEQ
(REL. 32, LAST ANN
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182
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llarity 93.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis_core;
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                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                               JS (SUBTYPE
VIRUSES; H
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24, LAST SEQUENCE UF
24, LAST ANNOTATION
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                                                                                                        s.,
                                                                                                        YOSHIDA
                                                                                                                                                                                               E ADW4 / STRAIN BRAZIL / ISOLATE W4B). HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E ADW2 VARIANT SF).
HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                                                                                                                                                                                                                    SEQUENCE UP
ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1314; DB 1;
Pred. No. 7.31e-219;
9; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                        C.F.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                new variant of hepatitis B virus
                                         B virus
subtype
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                                                                                                           GASPAR A.M.C.,
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                                           (HBV) genotype adw4.";
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SEQUENCE
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           HARRISON T.J.;
"The complete nucleotide sequence of the genome of a hepatitis virus isolated from a naturally infected chimpanzee.";
J. GEN. VIROL. 69:1383–1389(1988).
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                                                                                                                                                                                        entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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                                                                    PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                                EMBL; D00220; D1000603; -. PIR; A28885; NKVLCP.
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212 AA;
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    183 AA;
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(REL. 12, LAST SEQUENCE UPDATE)
(REL. 14, LAST ANNOTATION UPDATE)
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larity 92.9%;
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Best Local :
                 CORA_HPBV9
P17099;
01-AUG-1990
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CORE ANTIGEN
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01-AUG-1992
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SEQUENCE
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(IN) FIELD B.N., JAENISCH
ANIMAL VIRUS GENETICS, PP.
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P03148;
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177; Conservative
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185 AA;
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21304 MW;
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23, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDAT
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94.5%;
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LAST SEQUENT LAST ANNOTED
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Pred. No. 3.94e-217;
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Pred. No. 1.04e-217;
6; Mismatches 4:
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                                                                                                                                             SEQUENCE FROM N.A. SPECIES-WOODCHUCK HEPATITIS VIRUS 7, MEDLINE; 88101359.
                                                                                                                                                                                                                                                                                  "Nucleotide sequence of a cloned woodchuck hepatitis virus comparison with the hepatitis B virus sequence.";
J. VIROL. 41:51-65(1982).
                                                                                                                                                                                                                                                                                                                                                                                                  GALIBERT F., CHEN T.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. SPECIES-WOODCHUCK HEPATITIS VIRUS MEDLINE; 82216969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS WOODCHUCK HEPATITIS VIRUS
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REPEAT 193 200
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KOECHEL H.G., SCHUELER A., LOTTMANN S., THOMSSEN R.;
SUBMITTED (FEB-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRUSES;
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                                                                                                           COHEN J.I., MILLER
                                                                          PURCELL R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172
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Sequence comparison of hows conservation of
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11 Similarity 95.2%;
177; Conservati
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TIS VIRUS 7 (WHV 7),
TIS VIRUS 7 (WHV 59), AND
TIS VIRUS 8 (INFECTIOUS CLONE) (WHV 8).
VIRUSES: HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
                                                                                                        R.H.,
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of woodchuck hepatitis f the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                      MANDART E.;
                                                                                                           ROSENBLUM
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HEPADNAVIRIDAE;
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Pred. No. 6.14e-217;
5; Mismatches 2;
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                                                                                                        в.,
                                                                                                                                                                                  AND WOODCHUCK HEPATITIS VIRUS
                                                                                                           DENNISTON K.,
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e; orthohepadnavirus
                             virus
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                                                                                                           GERIN J.
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Best Local S
Matches 12
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EMBL; M18752; G336140; -.
EMBL; M18752; G336145; -.
EMBL; J04514; G336149; -.
PIR; A03713; NKVLC.
PIR; C32397; NKVLC4.
PIR; C32397; NKVLC4.
PIR; C32397; NKVLC4.
                                                                                                                                                                                                                                                                                                                          CORA_HPBGS STAN
P03153;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
01-JAN-1990 (REL. 1
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                                              SEQUENCE FROM N.A.

MEDLINE; 84267998.

SEEGER C., GANEM D., VARMUS H.E.;

SEEGER C., GANEM D., VARMUS H.E.;

STOUCHOOTICLE SEQUENCE OF an infectious

ground squirrel hepatitis virus.";

J. VIROL. 51:367-375(1984).
  This
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PIR; C32397; NKVLC4.
PIR; C32397; NKVLC3.
PFAM; PF00906; Hepatitis_core;
CORE PROTEIN; REPEAT.
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SPECIES-WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
                                                                                                                                                                                                                           GROUND SQUIRREL HEPATITIS VIRUS (GSHV). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                        CORE ANTIGEN
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larity 67.0%;
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01, LAST SEQUENCE UPDATE)
13, LAST ANNOTATION UPDATE
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copyright.
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Pred. No. 5.57e-147;
25; Mismatches 32;
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Query Match 42.3%;
Best Local Similarity 66.3%;
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                       PIR; A03714; NKVLC2.

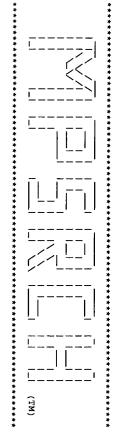
PFAM; PF00906; Hepatitis_core;

CORE PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KODAMA K., OGASAWARA N., YOSHIKAWA H., MURAKAMI S.;
"Nucleotide sequence of a cloned woodchuck hepatitis virus
evolutional relationship between hepadnaviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A03715; NKVLS.
PFAM; PF00906; Hepatitis_core;
                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                 EMBL; M11082; G336135; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 86062931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORA_WHV8
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Local Similarity 68.1%;
les 128; Conservative
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174
187 AA;
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204
217 AA;
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(REL. 06, LAST SEQUENCE UPDATE)
(REL. 12, LAST ANNOTATION UPDATE)
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211
; 25189 MW;
                                                                                                            21579 MW; A1C354F3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 (WHV 8).
HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
Score 933; DB 1; L4
Pred. No. 4.94e-146;
26; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 934; DB 1; Le
Pred. No. 3.20e-146;
22; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                            61
                                                                                                     1 MDIDPYKEFGSSYQLLNFLPLDFFPDLNALVDTATALYEEELTGREHCSPHHTAIRQALV
 QSRESQC
                OSPSANC 187
                               CWDELTKLIAWMSSNITSEQVRTIIVNHVNDTWGLKVRQSLWFHLSCLTFGQHTVQEFLV
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Search completed: Thu Dec 16 13:49:59 1999 Job time: 33 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 16 13:50:17 1999; MasPar time 20.79 Seconds 774.478 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US3890-10-38183 (1-295) from us3890-10-38183.pep 2205 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 295

Scoring table: PAM 150 Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.681; Variance 107.222; scale 0.435

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	% Query Match	Length	BB	Ħ	Description		Pred. No.
ы	1375	62.4	212	14	Q89656	PRE-C/CORE.		2.79e-219
2	1373		183	14	Q89437	X, PREC AND C GENES (	C	6.48e-219
ω	1373		183	14	800890	AND C GENES (	'n	
4	1374		212	14	Q68020	ORE.		4.25e-219
Ç	1374	62.3	212	14	Q89597	HBCAG.		4.25e-219
S	1373	62.3	212	14	Q67876	PRE C/C ORF.		6.48e-219
7	1372	62.2	212	14	011884	CORE ANTIGEN PRECURSOR	Ħ	9.87e-219
8	1370	62.1	183	14	Q68066	X, PREC AND C GENES (	Ê	2.29e-218
9	1370	62.1	212	14	Q68068	ORE.		2.29e-218
10	1370	62.1	212	14	Q68025	PRE-C/CORE.		2.29e-218
11	1369		212	14	Q67872	PRE C/C ORF.		3.49e-218
12	1369		212	14	Q67984	PRE-C/CORE.		3.49e-218
13	1369		212	14	Q68032	PRE-C/CORE.		3.49e-218
14	1368		212	14	Q68010	PRE-C/CORE.		5.32e-218
15	1366		212	14	Q68070	PRE-C/CORE.		1.24e-217
16	1366	62.0	212	14	Q68030	PRE-C/CORE.		1.24e-217
17	1364		183	14	Q67989	X, PREC AND C GENES (	Z	2.87e-217
18	1363		183	14	Q68048	X, PREC AND C GENES (	H	4.37e-217
19	1363	61.8	212	14	Q68014	PRE-C/CORE.		4.37e-217
20	1363	61.8	212	14	Q68012	PRE-C/CORE.		4.37e-217

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
1341	1341	1341	1341	1342	1343	1344	1344	1345	1347	1348	1348	1349	1351	1351	1352	1355	1357	1357	1359	1360	1360	1360	1362	1363
•	60.8	•	•	٠	60.9	•	٠	•	61.1	61.1	61.1	61.2	61.3	61.3	61.3	61.5	61.5	61.5	61.6	61.7	61.7	61.7	61.8	61.8
212	212	183									183										212	212	212	212
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	7
Q81115	Q68042	Q68003	268064	Q67964	Q68023	Q68035	092918	Q67973	267912	Q68060	Q68037	Q67997	Q89719	Q67946	Q89531	Q68045	Q68077	Q68075	Q68053	Q96845	268016	Q89446	Q680 <b>5</b> 1	Q67980
HBEAG, HBCAG.	PRE-C/CORE.	X, PREC AND C GENES (S	C GENES	C GENES	O C GENES	PRE-C/CORE.	IN PREC	X, PREC AND C GENES (T	RE PROTEI	GENES (	X, PREC AND C GENES (D	X, PREC AND C GENES (B	PRE-C/CORE.	C ANTIGEN.	CORE PROTEIN.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	COMPLETE GENOME.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.
4.62e-213	4.62e-213	4.62e-213	4.62e-213	3.03e-213	1.99e-213	1.31e-213	1.31e-213	8.57e-214	3.69e-214	2.42e-214	2.42e-214	1.59e-214	6.85e-215	6.85e-215	4.50e-215	1.27e-215	5.48e-216	5.48e-216	2.36e-216	1.55e-216	1.55e-216	1.55e-216	6.67e-217	4.37e-217

SQ.	DR	DR	DR	DR	DR	DR	DR	DR	DR	RL	RA	RA	RP	RN	2:	3	RT	RA	R R	R	RL	RA	RC	ŖΡ	RN	RL	RA	R	ŖΡ	RN	გ	S	GN	DE	D	ij	Di	AC	IJ	RESULT
SEQUENCE 212 AA; 24350 MW; 71EA2C82 CRC32;	PFAM; PF00906; Hepatitis_core; 1.	G7361	J02203;	235716;	x85306;	x85283;	X85313;		x85290; G736116;	1. 279:386-390(1985).	TSIBINOGIN V.V., KUKAIN R.A.;	BORISOVA G.P., PUMPEN P.P., BYCHKO V.V., PUSHKO P.M., KALIS Y.V.,	SEQUENCE FROM N.A.				ide sequence of the hepatitis B virus genome (subty	F., MANDART	MEDLINE; 81012091.		SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.	ZAK A.;	STRAIN=AYW4;	SEQUENCE FROM N.A.	•	(MAR-1995) TO EMBL/GENBANK/DDBJ DATA E	LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;	20	SEQUENCE FROM N.A.		ET	HEPATITIS B VIRUS.	PRE-C/CORE.		08, LAST ANNOTATIO	(TREMBLREL. 01,	(TREMBLREL.		Q89656 PRELIMINARY; PRT; 212 AA.	LT 1

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Q89437;
Q89437;
Q1-NOV-1996 (TREMBLREL. 01, CI
01-NOV-1996 (TREMBLREL. 01, LJ
01-NOV-1998 (TREMBLREL. 08, LJ
x, PREC AND C GENES (CASTAA 2
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SUBMITTED (DEC-1995)
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
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Pred. No. 2.
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No. 2.79e-219;
Mismatches 0;
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. No. 6.48e-219;
Mismatches 0;
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X, PREC AND
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X85291; G736119; -.
EFFAM; PF00906; Hepatitis_core; 1.
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PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 183 AA; 21102 MW; BBE9AFBB CRC32;
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VIRUSES; R
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HEPATITIS B VIRUS.
HEPATITIS DETROID VIRUSES;
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                                                                                                                                                                                                                                                                   SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 171
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C GENES (FERRACUTI 1).
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                                                                                                                                                                                                                                                                                                                                                                                        Score 1374; DB 14;
Pred. No. 4.25e-219;
2; Mismatches 0;
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Pred. No. 6.48e-219;
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O1-NOV-1996 (TREMBLREL 08,
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PRE C/C ORF.
HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES; H
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SEQUENCE FROM N.A.
STRAIN-PATIENT CI, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (SEP-1995) TO EMBL/GI
EMBL; X72702; G288930; -.
EMBL; X80925; E198084; -.
PFAM; PF00906; Hepatitis_core;
SEQUENCE 212 AA; 24336 MW;
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MEDLINE; 94079539.
PREISLER-ADAMS S., SCHLAYER M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KARAYIANNIS
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Pred. No. 4.25e-219;
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Best Local S
Matches 18
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Best Local S
Matches 18
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01-JUL-1997 (TREMBLREL. 04, L
01-NOV-1998 (TREMBLREL. 08, L
CORE ANTICEN PRECURSOR.
HEPATITIS B VIRUS.
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RAO B.S., CASEY J.L., RINAUDO J.
SUBMITTED (MAR-1997) TO EMBL/GEN
EMBL; U95551; G2182120; -
PFAM; PF00906; Hepatitis_core; 1
SEQUENCE 212 AA; 24360 MW; 7
                                         Q68066;
Q68066;
Q1-NOV-1996
Q1-NOV-1998
Q1-NOV-1998
X, PREC AND
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011884;
01-JUL-1997
01-JUL-1997
01-NOV-1998
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EMBL; X65258; G59436; -.
PFAM; PF00906; Hepatitis_core;
SEQUENCE 212 AA; 24348 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /IRUSES; RETROID VIRUSES;
                                                                                                                                                                                                                                                                      209
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182; Conser
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                                         (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLEL. 08, LAST ANNOTATION UPDATE)
C GENES (LICHERI 2).
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larity 98.9%;
Conservative
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llarity 98.9%;
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TO EMBL/GENBANK/DDBJ
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Pred. No. 6.48e-219;
2; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 9.87e-219;
2; Mismatches 0;
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6ED741BE CRC32;
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DATA BANKS
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Best Local S
Matches 18
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Best Local Similarity
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85314; G736504; -.
PFAM; PF00906; Hepatitis_core; 1.
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85315; G736207; -.
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PRE-C/CORE.
HEPATITIS B VIRUS.
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01-NOV-1998
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01-NOV-1996
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                                                                 ESQC
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5 (TREMBLREL.
9 (TREMBLREL.
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larity 98.9%;
Conservative
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  PRELIMINARY;
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98.4%;
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Pred. No. 2.29e-218;
3; Mismatches 0;
                                                                                                                                                                                                                         Score 1370; DB 14;
Pred. No. 2.29e-218;
1; Mismatches 1;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
  PRT;
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SEQUENCE FROM N.A.
STRAIN-PATIENT C, HBSAG POSITIV, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., P.
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X65257; G59431; -
EMBL; X65257; G59431; -
EPRAN; PF00906; Hepatit1s_core; 1.
PFAN; PF00906; Hepatit1s_core; 1.
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Q67872;
Q1-NOV-1996
01-NOV-1996
01-NOV-1998
PRE C/C ORF.
HEPATITIS B
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01-NOV-1996
01-NOV-1998
01-NOV-1998
PRE-C/CORE.
PRE-C/CORE.
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SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X85293; G736126; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;
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                                       VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYL 148
                                                                                                                                                                                                                                                                                          l Similarity 98.4%;
181; Conservative
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                                                                                                                                                                                                                                                                                                             62.18;
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                                                                                                                                                                                                                                                                                        Score 1369; DB 14;
Pred. No. 3.49e-218;
2; Mismatches 1;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 2.29e-218
1; Mismatches 1
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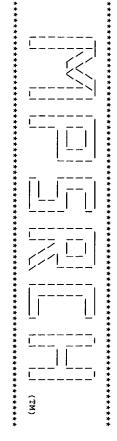
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Matches 18
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Best Local (
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01-NOV-1996 (TREMBLREL. 0.
01-NOV-1998 (TREMBLREL. 0.
PRE-C/CORE.
PRE-C/CORE.
HEPATITIS B VIRUS.
VIRUSES; RETROID VIRUSES;
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01-NOV-1996
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Q68032
Q68032;
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Q67984;
                                                                                                                                                                                                                           STRAIN-PATIENT CHIGHINE-2'86;
LAMIM.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.; SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85296; G736139; -
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24308 MW; 69D87B53 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-PATIENT VITTORINA'92;
TAT M E MAZZOLENI A.P., PORRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRE-C/CORE.
HEPATITIS B VIRUS
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mes 181; Conser
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                     LCWGDLMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFKQLLWFHISCLTFGRETVIEYL
                                                           ESQC 212
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62.18;
1 Similarity 98.98;
182; Conservation
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larity 98.4%;
Conservative
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Pred. No. 3.49e-218;
1; Mismatches 1;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                            Score 1369; DB 14;
Pred. No. 3.49e-218;
3; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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83D9780B CRC32;
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Query Match
Best Local Similarity
Matches 182; Conser
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Q68010;
01-NOV-1996
01-NOV-1998
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01-NOV-1996
01-NOV-1996
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LAI M.E. MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85285; G736100; -.
PFAM; PF00906; Hepatitis_core: 1.
SEQUENCE 212 AA; 24292 MW; 04A4D12D CRC32;
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                                                                                                                              STRAIN-PATIENT GIORDO'84;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA B
EMBL; X85316; G736210; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24376 MW; 80F52D0F CRC32;
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PRE-C/CORE.
HEPATITIS B VIRUS
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HEPATITIS B VIRUS.
HEPATOLIS B VIRUSES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181;
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Similarity 98.4%;
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(TREMBLREL.)
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(TREMBLREL.
62.0%;
larity 98.9%;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
Score 1366; DB 14;
Pred. No. 1.24e-217;
1; Mismatches 1;
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Pred. No. 5.32e-218;
2; Mismatches 1;
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δõ Вb Qy δõ Вp Дb Qy Search completed: Thu Dec 16 13:52:01 1999 Job time :  $104\ \text{secs}$ . Db 209 ESQC 212

US3890-1-38183
MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGELMTLAT
MVGVNLEDPASRDLVVSYVURIITRDGFLLLQMDFGFPEHLLVDFLQSLSMDIDPYKEFGATVELLSFLP
SDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGELMTLATWVGVNLEDPASRDLVVSYVN
TNMGLKFRQLLWFHISALYREALESPETVIEYLVSFGVWIRTPPAYRPNAPILSTLPETTVVRRRGRSPRRRT
PSPRRRRSQSPRRRRSQSRESQC1

زمن



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:32:26 1999; MasPar time 13.80 Seconds
467.015 Million cell updates/sec

Description: Perfect Score: Title:

Sequence: >US3890-1-38183 (1-303) from us3890-1-38183.pep. 2263 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 303

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 33.516; Variance 173.687; scale 0.193

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

11000000000000000000000000000000000000	Result
1375 1375 1375 1363 1358 1358 1358 1344 13344 13334 13334 13334	Score
59.14 59.16 59.16 59.16 59.16 59.17 59.16	Query Match
194 346 184 193 183 183 183 183 183 184 208 196 196 183 183	Length
332 332 332 332 332 332 332 332 332 34 44	B
W50242 W50240 R27473 P80959 P80951 W50241 W50241 W50241 W69044 R05635 P000041 R40808 P40808 R40808 R40808 R40808 R40808	ID
Hepatitis B virus pre Hepatitis B virus sub Hepatitis B virus sub Hepatitis B virus pre Hepatitis B virus core Hepatitis B virus core Hepatitis B virus core Hepatitis B antigen. Sequence of core antiplasmid phBv DN AA en Sequence of core / PV Hepatitis B core / PV Hepatitis virus core Hepatitis B core prot Hepatitis B core prot Hepatitis B core prot Hepatitis B core prot	Description
6.72e-100 6.72e-100 6.72e-100 6.49e-99 1.38e-98 1.67e-98 4.29e-98 9.14e-98 9.14e-98 9.14e-98 7.30e-97 7.30e-97 7.30e-97 1.55e-96 1.55e-96	Pred. No.

45	44	3	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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183	w	w	œ	203	214	185	185	185	185	185	185	185	ω	w	185	185	w	u	185	185	S	5	9	214	ω	ω	198	183
17	7	17	32	ب	ш	σ	0	σ	σ	σ	σ	σ	13	13	σ	σ	13	26	σ	σ	10	σ	20	μ.	13	10	œ	12
R98884	89.8	887	025	287	960	980	078	102	980	980	102	078	887	886	102	078	886	900	102	078	528	980	904	070	986	528	080	σ
itis B viru	titis B virus E	titis B virus E	patitis B virus p	Ag/beta-Gal fusio	core antige	dified hepatitis	ered HBcAg protei	tered HBcAg prot	patitis B core ant	dif	ered HBcAg pro	tered HBcAg prote	patitis B virus	patitis B virus p	HBcAg prote	tered HBcAg protei	atitis B virus	antigen of HB	ive HBcAg prote	cAg prote	duced sequence of	epatitis B core ant	PHBV DN BB e	duced amino acid s	titis B virus po	11 length c	titis B	titis B Virus c
2.64e-9	196-9	.03e-9	.11e-9	.55e-9	.42e-9	.11e-9	.11e-9	.11e-9	.75e-9	.20e-9	.20e-9	.20e-	.20e-9	.79e-9	.85e-9	.85e-9	.19e-9	.81e-9	.03e-9	.03e-9	.03e-9	.03e-9	.51e-9	.51e-9	.51e-9	.83e-9	.88e-9	.55e-9

	CC inserted into t	/see w50	replicat											inhibition of			WPI; 98-1933	Melegari M	(GEHO ) GEN	03-SEP-1996;	03-SEP-19 <b>97</b> ;	N W09809649-A1				Synthetic.	Hepatitis B		Viral repli	28-SED-1998	#50242.	ID W50242 standard:	FOIT TO 1
proteins can be produced by recombinant methods using claimed exogenously	The	IN (see W50236), Met-p18 (see W50237) and Met-p18-Het	Suitable inhibitory proteins include p25 (see W50250),	of them, leads to transdominant inhib.	Thus, over-expression of the precore proteins, or	thereby render the nucleocapsids deficient in encapsidating HBV	incorporated into HBV nucleocapsids along with the p21 core protein	precore or precore-related proteins. These proteins can be	that HBV replication is inhibited in the presence of high levels of	full-length HBV precore protein (see W50250). Evidence is provided	elimination of the 19-amino acid leader peptide from the 25 kDa	This polypeptide comprises the hepatitis & virus (HBV) 22 kDa (p22)	Claim 11; Page 40; 60pp; English.	inhibition of viral replication, especially hepatitis B virus	subunit(s) into a viral nucleocapsid - useful for	DNA encoding proteins which can be incorporated with wild type	, , , , , , , , , , , , , , , , , , ,	alions by wands IP:	HOSPITAL CORP	US-025370.	U15500.	1 11000	/lahel= n22	2194	Location/Qualifiers			Met-p22.	inhibitor; HBV; nucleocapsid;	trat potru		: Protein: 194 AA.	

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PF 03-SEP-1996; US-025370.

PR 03-SEP-1996; US-025370.

RE 03-SEP-1996; US-025370.

RE 03-SEP-1996; US-025370.

RE 04-19325/17.

PR WPI; 98-193325/17.

DAA encoding proteins which can be incorporated with wild type of the subunit(s) into a viral nucleocapsid - useful for nucleocapsid subunit(s) into a viral nucleocapsid - useful for nucleocapsid subunit(s) into a viral nucleocapsid - useful for this page 35, 60pp; English.

Claim 15; Page 35; 60pp; English.

Claim 15; Page 36; 60pp; English.

Construct hat is encoded by the full-length HBV precore of precore gene.

Claim 15; Page 35; 60pp; English.

Claim 15; Page 35; 60pp; English.

Claim 15; Page 36; 60pp; English.

Claim 15; Page 37; 60pp; English.

Claim 15; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 18
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Matches
                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus precore p25 p
Viral replication; inhibitor; H
hepatocyte; liver; p25 protein.
Hepatitis B virus.
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    120
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                                        29
                                                                                                  Local
ESQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lcwgelmtlatwvgvnledpasrdlvvsyvntnmglkfrqllwfhiscltfgretvieyl 130
                                                                            ch 60.8%; l Similarity 99.5%; 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
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larity 99.5%;
Conservative
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Pred. No. 6.72e-100;
1; Mismatches 0;
                                                                            Score 1375; DB 32;
Pred. No. 6.72e-100;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide.
HBV; nucleocapsid; gene therapy;
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                                                                                                                  Length 212;
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                                                                                                                                                                                      DR WP1; 92-331/80/40.

BR W-PSDB; 029105.

PT Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating against viral infections such as rables, hepatitis B, PT Waccine comprises recombinant, attenuated pox-virus - use for vaccinating against viral infections such as rables, hepatitis B, PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 456pp; English.

The sequence given is encoded by an expression cassette which comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/CCC) which is precisely linked to the I3L promoter derived from vaccinia virus. This DNA sequence was linked to the S1 and S2 core) which is precisely linked to the I3L promoter derived from vaccinia virus. This DNA sequence was linked to the S1 and S2 recombinant expressing the HBV gene. Other HBV genes were also used in the construction. These were HBV M protein (small pre-S antigen, spsAg). Each of these gene sequences were inserted individually into three different sites of NYVAC separated by from each other by large regions of vaccinia DNA containing essential genes. NYVAC is a Copenhagen vaccine strain of vaccinia virus which has been modified by deletion of six non-essential regions of the genome encoding known or potential virulence factors.
               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09215672-A.

17-SEP-1992.

17-SEP-1992.

07-MAR-1991; US-666056.

11-JUN-1991; US-666056.

11-JUN-1991; US-713967.

(VIRO-) VIROGENETICS CORP.

(VIRO-) VIROGENETICS CORP.

COX WI, De Taisne C, Francis J, Gettig RR, Johnson GP,

Limbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus SE,

Riviere M, Tartagila J, Taylor J;

WPI; 92-331718/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 3
R27473 standard; Protein;
R27473;
                                                                                                                 The deletion loci were engineered as recipient loci for the insertion of foreign genes. The spacing of the three inserted sequences ensured that any recombination that did occur would lead to disruption of the vaccinia genome and would cause unviable vaccinia virus. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg; vaccinia virus; I3L; promoter; NYVAC; recombinant; HBV L; large pre-S antigen; 1psAg; fusion protein; pre-S region; S12/s1; S2; Copenhagen vaccine strain; vaccinia virus; virulence fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1993 (first entry)
S12/core protein.
Hepatitis B virus; HBV; M
vaccinia virus; I3L; prom
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 60.8%; larity 99.5%; Conservative
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109..163
/label S2
164..346
/label Cor
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                     1375; DB 5;
No. 6.72e-100;
                                     Length 346
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ULT 5
W50241 standard;
W50241;
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This sequence contains the T cell stimulating epitopes, amino acid residue 1-55 and 70-140. It is believed that the regions 1-44 and 70-140 do not contain determinants that suppress T cell activation. Polypeptides essentially consisting of 15 to 55 amino acids corresponding to the above mentioned HBV regions are T cell stimulating. Coupling a polypeptide immunogen to such sequences, e.g. by using a bifunctional reagent which forms a disulphide link, improves its immunogenicity. These are useful in vaccines and can be therapeutically to improve T cell response to HBCAg in infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wPI; 88 163287/24.

New conjugates and fusion proteins of immunogenic polypepytide and hepatitis B core antigen and T cell stimulating polypeptide coresp. to core_antigen, useful in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1987; 310725.
07-OCT-1987; US-106538.
07-OCT-1987; US-939617.
(SCRI-) Scripps Clinic Res.
Thornton GB, Moriarty AM, Millich DR, McLachlan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus subtype ayw. core protein.
Conjugate; fusion protein; hepatitis B core protein; HBV subtype ayw.;
T cell stimulating polypeptide; vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subjects.
See also P80896-P80898 and P80951-P80859
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                                 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1363; DB 1;
Pred. No. 6.49e-99;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22) protein that is produced by elimination of the 19-amino acid leader peptide from the 25 kDa full-length HBV precore protein (see w50250). Evidence is provided that HBV replication is inhibited in the presence of high levels of HBV precore or precore-related proteins. These proteins can be incorporated into HBV nucleocapsids of component, and thereby render the nucleocapsids deficient in encapsidating HBV pregenomic RNA. Thus, over-expression of the precore proteins, or certain variants of them, can be incorporated into HBV nucleocapsids of the inhibitory proteins, or certain variants of them, can be precore proteins, or certain variants of them, can be produced p25 (see W50250), p22, Met-p22 (see W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18 (see W50237), p18 (see W50236), Met-p18 (see W50237) and Met-p18 (see W50238), May be inserted into the p22 and Met-p22 polypeptides. The inhibitory proteins can be produced by recombinant methods using claimed expression vectors and host cells. They can be provided exogenously to the target cells for use in inhibiting HBV replication.

Alternatively, a nucleic acid construct that directs overexpression of an inhibitory protein in target cells is used for the gene therapy of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
   w50251;
28-SEP-1998 (first entry)
Hepatitis B virus p21 core protein.
Viral replication; inhibitor; HBV; nucleocapsid;
hepatocyte; liver; p21; core protein.
Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding proteins which can be incorporated with wild type nucleocapsid subunit(s) into a viral nucleocapsid - useful for inhibition of viral replication, especially hepatitis B virus Claim 9; Page 34-35; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Melegari M, Scagl
WPI; 98-193325/17
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                                                                                                                                       T 6
W50251 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                       SMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAI 179
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|larity 98.4%;
|Conservative
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                                                                                                                                         Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1359; DB 32;
Pred. No. 1.38e-98;
2; Mismatches 1
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                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 193;
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CC This is the 21 kDa (p21) protein of hepatitis B virus (HBV) that CC assembled into a 180 kSa subunit nucleocapsid structure that CC promotes viral replication. Evidence is provided that HBV CC precore or precore-related proteins. These proteins can be concerned into HBV nucleocapsids along with the p21 core protein can determine the nucleocapsids deficient in encapsidating HBV CC and thereby render the nucleocapsids deficient in encapsidating HBV cc pregenomic RNA. Thus, over-expression of the precore proteins or CC ertain variants of them, leads to transdominant inhibition of HBV CC preplication. Suitable inhibitory proteins include p25 (see W50250), p22 (see W50241), Met-p22 (see W50234). These proteins CC can be produced by recombinant methods using claimed expression CC vectors and host cells, and can be provided expensity to target CC ells for use in inhibiting HBV replication. Alternatively, a concleic acid construct that directs overexpression of an inhibitory conference in faction.
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Best Local
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12-MAR-1998.
13-SEP-1997; U15500.
03-SEP-1996; US-025370.
(GEHO ) GEN HOSPITAL CORP.
Mellegari M, Scaglioni PP, W
WPI; 98-193325/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus core protein.
Hepadhavirus; HBV; woodchuck hepatitis virus; hepatitis ground squirrel hepatitis B virus; duck hepatitis B virus core protein; replication; antiviral; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09044;
11-APR-1997
                                        misc_difference
                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09044 standard; Protein; 183
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                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 71..180
                                                                                                                                                                                              polypeptides
81..180
                                            polypeptides
171..180
                                                                                                                 acid position
                                                                                                                                                                                                                              /note= "C-terminus of core protein is at any
acid position between 71-180 in mutant
polypeptides of the invention (Claim 23)"
    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "immunodominant region"
                                                                                                                                                             /note=
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                                                                        "C-terminus of core proposition between 81 and options of the invention of
    "C-terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wands
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Pred. No. 1.67e-98;
1; Mismatches 1.
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                                                                        core protein is at a 81 and 180 in mutant nvention (Claim 5)"
    core protein
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virus;
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(GEHO) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
WPI; 97-087176/08.
N-PSDB; T49594.
           Hepatitis B antigen.
Hepatitis B virus; va
Synthetic.
EP-374869-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9700698-A1.
09-JAN-1997.
20-JUN-1996; U10602.
20-JUN-1995; US-0178.
                                                                                                                                                                                                                                                                                                                                                                                                  hepatitis B virus (HBV) or other hepadnavirus creates a mutant polypeptide capable of reducing replication of the wild-type virus by a dominant negative mechanism. The inhibitory effect is species-specific and is achieved by deletion of a few C-terminal amino acids from the core protein, and/or by joining the core protein to a hepadnavirus surface protein (see also W09045), creating a core-surface fusion. Such mutant polypeptides (see also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
                                                                     R05635 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New method for inhibiting the replication of hepadnaviruses -
comprises introducing a mutant polypeptide with a mutated core
protein or corresponding nucleic acid, for treating, e.g. hepatitis
                                                           30-OCT-1990
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Alteration of the C-terminus of the core protein (W09044)
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181; Conser
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larity 98.9%;
Conservative
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminus of core protein is a position 178 in mutant polypeptides of invention (Claim 7)"

ce 172...183 /note= "amino acid residues 172-183, pi are deleted from the core protein in mu polypeptides of the invention"
                                                                                                                                                                                                                                                                                                                                                                               ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid position between 174 and 180 i polypeptides of the invention (Clai 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides of the 174..180
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                                                                                                                                                                                                                                                                                                                                          Score 1353;
Pred. No. 4
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(Claim
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                                                           Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Example: Figs 3-4; 43pp; English. Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-conty, pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HBIO1/pBR322-Pst I dG: Tetr AmpS HBV+.
                                                                                                                                                                                                                                                                         14-OCT-1992 (first entry)
Sequence of core antigen.
Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
EP--13828-A.
06-AUG-1980.
21-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA encoding Hepatitis B virus polypeptide antigens used in detection of infection and in vaccine production. Disclosure: 4pp: English.

Polypeptide fragments encoded by the DNA sequence are antigenic for the BNA and may be used as a vaccine or in detection. Peptides may be cultured in a suitable bacterial host such as E.coli.

Fragments of the sequence are also claimed as being antigenically useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOJ) Biogen Inc.
Murray K, Schaller HE;
WPI; 90-195067/26.
                                                                                                                                                                                                                           N-PSDB; N00003.
                                                                                                                                                                                                                                      (BIOJ ) BIOGEN NV.
Murray K, Schaller HE;
WPI; 80-57268C/33.
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22-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
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177; Conser
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177; Conser
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59.6%;
(larity 96.7%;
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Score
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5; N
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Pred. No. 9.14e-98;
5; Mismatches 1
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re 1349; DB 5;
1. No. 9.14e-98;
Mismatches 1;
                       Length 183;
Indels
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Best Local :
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09-JAN-1997
20-JUN-1996; U10602.
20-JUN-1995; US-017814.
(GEHO ) GEN HOSPITAL CORP.
Melegari M, Scaglioni PP,
WPI; 97-087176/08.
                                                                                                                                                                                                                                                                                                                                            Plasmid phby DN Ac carries an insert (T49598) coding for a prot (W09048) comprising a hepatitis B virus (HBV) core protein (set also W09044) fused in-frame at amino acid 179 with the HBV suri protein (see also W09045) at amino acid 8. Plasmid phby DN BB (T49599) expresses the HBV core fused at amino acid 175 to the surface protein at amino acid 112 (W09049). PHBV DN AA was at least as potent an inhibitor of HBV replication as construct PHBV DN (T49597); PHBV DN BB was less inhibitory than PHBV DN. Vectors expressing hepadnavirus dominant negative core mutants be utilised in the gene therapy of viral infections.
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Plasmid pHBV DN AA encoded HBV dominant negative polypeptide.
Hepaddnavirus; woodchuck hepatitis virus; hepatitis delta viru
HBV; ground squirrel hepatitis B virus; duck hepatitis B viru
core protein; replication; antiviral; gene therapy; pHBV DN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T49598.

New method for inhibiting the replication of hepadnaviruses comprises introducing a mutant polypeptide with a mutated or protein or corresponding nucleic acid, for treating, e.g. ht
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l Similarity 100.0%;
179; Conservative
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d. No. 2.35e-97;
Mismatches 0;
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Matches 17
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Hepatitis B c
Hepatitis B;
Synthetic.
Key
J05192170-A.
03-AUG-1993.
24-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation Claim 13; Page 40; 43pp; English. Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contry pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973). The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977). It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dG:
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Sequence of core antigen: antibody: diagnosis; vaccine.
Hepatitis B virus;
EP--13828-A.
06-AUG-1980.
21-DEC-1978; GB-049907.
27-DEC-1978; GB-050039.
01-NOV-1979; GB-037910.
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14-OCT-1992 (fir
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                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 208
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B core / PV-1 /
B; core; HBC; PV
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26..208
/label= HBC
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20..25
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96.2%;
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Pred. No. 7.30e-97;
5; Mismatches 1
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WPI; 93-277479/35.

N-PSDB; Q47738.

Recombinant plasmid for high immunogenity virus - contains recombined haemagglutinin gene, hepatitis B core gene of vaccinia virus and exotic genes
Disclosure; Fig 9; 12pp; Japanese.

The hepatitis B core gene is recombined with PV-1 DNA and IL-1 beta to form a plasmid (047738) which is then used to propose the process.

NB: Sequence is difficult to read in the original
                                                                                                                                                                                                                                                                            Recombinant plasmid for high immunogenity virus - cont recombined haemagglutinin gene, hepatitis B core gene virus and exotic genes. Disclosure; Fig 7; 12pp; Japanese.

The hepatitis B core gene is recombined with PV-1 DNA and IL-1 beta to form a plasmid (Q47738) which is ther a vaccine. NB: Sequence is difficult to read in the or
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R40806 standard; Protein; 196
R40806;
16-FEB-1994 (first entry)
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Sequence 196
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(NISW) NISSHIN OIL MILLS
WPI; 93-277479/35.
N-PSDB; Q47736.
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Sequence 208
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24-SEP-1991;
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lcwgelmnlatwvgsnledpasrelvvsyvnvnmglkirqllwfhiscltfgretvleyl 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ch 59.1%;
l Similarity 94.6%;
175; Conservative
                                                                                                                                        ch 59.0%;
l similarity 95.1%;
175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
core / PV-1 fusion
; core; HBC; PV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP-243800
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                                                                                                                                                                                                                                      AA,
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14..196
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 7..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1337; DB 8; 1
Pred. No. 8.82e-97;
7; Mismatches 3;
                                                                                                                                      Score 1336; DB 8; Pred. No. 1.07e-96; 6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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IDENTIFICATION OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT OF THE SULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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Best Local Similarity 95.6%;
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NUG-1992 (first entry)
Hepatitis virus core antigen.
HBcAg; vaccine; diagnosis; HBV in
HBCAG; vaccine; HBV in
J59074985-A.
J59074985-A.
J59074985-A.
J59074985-A.
J59074985-A.
J69074985-A.
J74074985-A.
J7407498-A.
J740748
                                                                                                                                      R40805;
16-FEB-1994 (first entry)
Hepatitis B core protein.
Hepatitis B yirus.
Hepatitis B virus.
J05192170-A.
03-AUG-1993.
24-SEP-1991; 243800.
24-SEP-1991; JP-243800.
(NISW ) NISSHIN OIL MILLS LT
WPI; 93-277499/35.
N-PBUB; 047735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA used in prevention of infections by hepatitis virus B - comprises structural gene of hepatitis virus adr B surface antigen coding gene and at least 1 virus core antigen structural gene. Disclosure; Fig 3; 13pp; Japanese.

The sequence is that of hepatitis virus core antigen (HBcAg). It can be used as a vaccine for the prevention of infections by hepatitis B virus (HBV) and also in the diagnosis of early stages of HBV infection. See also P40310.
Recombinant plasmid for high recombined haemagglutinin ger virus and exotic genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 15
R40805 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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P40311 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PV-1;
                                                                                                                                                                                                                                                             LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
                                                gene,
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Pred. No. 1.55e-96;
5; Mismatches 3;
                                                immunogenity
ne, hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-1 beta;
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                                                virus -
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Matches 17
                                                                                                                                                                                                   Disclosure; Fig 6; 12pp; Japanese.

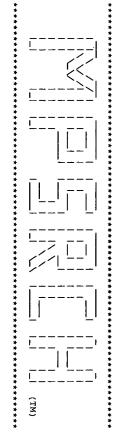
The hepatitis B core gene is recombined with PV-1 DNA and IL-1 beta to form a plasmid (047738) which is then used to a vaccine. NB: Sequence is difficult to read in the original specification.
                                                                                                                                                                                            Sequence
                                      301
                    181
                                                                             181
                                                                                                                  121
                                                                                               61
                                                                                                                sqc 183
                                                                                      CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
                                                                                                                                                      tch 58.9%;
al Similarity 95.6%;
175; Conservative
                                                                                                                                                                                             183 AA;
                                                                                                                                                      Score 1334; DB 8; Lo
Pred. No. 1.55e-96;
5; Mismatches 3;
                                                                                                                                                                         Length 183;
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Search completed: Thu Dec 16 13:35:27 1999 Job time: 181 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Thu Dec 16 13:35:44 1999; MasPar time 14.81 Seconds 820.017 Million cell updates/sec

Title:

Description:
Perfect Score:
Sequence: >US3890-1-38183 (1-303) from us3890-1-38183.pep 2263 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 303

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 47.447; Variance 117.780; scale 0.403

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Result No.
1373 1374 1374 1373 1370 1370 1370 1369 1369 1366 1366 1366 1366 1366 1366	Score 1375
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##residues 1-2 ##residues 1-2 ##cross-references ##experimental_sour #accession \$53264 ##molecule_type DNA ##residues 1-2 ##cross-references	##residues 1.2 ##residues 2.2 ##cross-references: ##cross-references: ##cxperimental_sour: ##ccession 53309 ##molecule_type DNA ##residues 1.2 ##cross-references: ##cross-references: ##cross-references:	##molecule_type DNA ##residues 1.2 ##cross.references   ##cxperimental_sour REFERENCE S53112 #authors Lai, M.E #submission submittee #accession S53191	REFERENCE #authors #submission #description #accession	DATE ACCESSIONS	RESULT 1 ENTRY TITLE ALTERNATE_NAMES CONTAINS ORGANISH ORGANISH
##molecule_type_DNA ##residues	##molecute_type_DNA ##residues_type_DNA ##cross-references_EMBL:X85283; NID:g736088; PID:g736090 ##cxperimental_source isolate patient Ferracuti'83 ##experimental_source isolate patient Ferracuti'83 ##molecule_type_DNA ##molecule_type_DNA ##rcsidues	##molecule_type DNA ##residues 1-212 ##label PLU ##residues 1-212 ##label PLU ##residues 1-212 ##label PLU ##residues 1-212 ##label PLU ##experimental_source subtype ayw4, isolate hb321 ##residues in its isolate hb321 ##residues	53277; NO3711 \$47404 Plucienniczak, A. Plucienniczak, A. Submitted to the EMBL Data Library, August 1994 Molecular cloning and sequencing of two complete genomes of pollsh isolates of human hepatitis B virus. \$47405	isolate patient Castey'83; isolate patient Ferrauct os; isolate patient Castey'83; isolate patient Sanna 84; isolate patient Licheri-1'85; isolate patient Flore-1'86; isolate patient Licheri'83 18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change 10-Oct-1997 \$47405; \$53191; \$53209; \$53234; \$53264; \$53249; \$53262;	hepatiti hers) pre-C/C

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#title Nature (1979) 281:646-650

#title Nucleotide sequence of the sequence of t
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#accession S53249
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##cross-references EMBL:X85306; NID:g736172; PID:g736174

##experimental_source isolate patient Flore-1'86

##experimental_source isolate patient Flore-1'86
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##residues 1-212 ##label LA6
##residues 1-212 ##label LA6
##coss-references EMBL:x85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
scession S53277
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##cross-references EMBL:X85317; NID:g736211; PID:g736214
##cross-references EMBL:X85317; NID:g736211; PID:g736214
##experimental_source patient Giordo-2-86
due to a stop codon between the alternative initiators
##note
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Local Similarity 99.5%;
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#formal_name hepatitis B virus, HBV
isolate patient Castaa-2'87
08-Jul-1995 #sequence_revision 03-Aug-1995
                                                                                                                                                        HBc antigen
                                                                                                                                                                                      core antigen -
Castaa-2'87)
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                                                                                                                      core antigen
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#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #stat
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##cross-references EMBL:X85291; NID:g736117; PID:g736119
##experimental_source isolate patient Castag-1'85
##experimental_source isolate patient Castag-1'85
##experimental_source isolate patient Castag-1'85
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##cross-references EMBL:X85289. IND:g736110; PID:g736113
##sxperimental_source isolate patient Castaa-2'87
##axperimental_source isolate patient Castaa-2'87
##axperimental_source isolate patient Castaa-2'87
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S53207
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(isolate patient Castag-1'85 and others)
HBC antigen; HBe antigen precursor / HBc antigen; pre-
                                                                                *superfamily hepatitis B virus core antigen alternative initiators; core protein
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Pred. No. 4.22e-202;

    Mismatches

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Data Library, March 1995
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##residues 1-212 ##label_prE
##cross-references_EMBL:X72702; NID:g288927; PID:g288930
##experimental_source_subtype_ayw, pattent_C1000
##experimental_source_subtype_ayw, pattent_C1000
##note due to a stop codon between the alternative_i
the e antigen precursor_cannot_be_produced
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#formal_name hepatitis B virus, HBV
subtype ayw, patient C1000
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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e antigen precursor / core antigen -
(subtype ayw, patient C1000)
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2; Mismatches 0;
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##cross-references EMBL:X65258; NID:g59434; PID:g59436
##experimental_source subtype ayw, patient CI
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#formal_name hepatitis B virus,
isolate patient Licheri-2'87
08-Jul-1995 #sequence_revision
                                                        HBc antigen
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y Match 60.5%;
Local Similarity 98.9%;
hes 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL 180
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S53270
S53112
Lai, M.E.; Mazzoleni, A
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S53112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e antigen precursor / core antigen • (isolate patient Castag'3)
HBe antigen precursor / HBc antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily hepatitis B virus core antigen core protein #length 183 #molecular-weight 21102 #chec
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                                                                                                                                                                                                                                                                                                                                             alternative initiators; core protein
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#formal_name hepatitis B virus, HBV
isolate patitent (astay'3
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                          #superfamily hepatitis B virus core antigen
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                                                                                                                                                                                        #product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #stat
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                                                                                                                                                           predicted #label ECP
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to the EMBL
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   Score 1370; Db 4,
bred. No. 1.36e-201;
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Pred. No. 1.36e-201;
3; Mismatches 0;
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Data Library, March 1995
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Data Library, March 1995
                                                               Length 212;
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Local Similarity 98.9%;
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                                                                                                                                                                                                                                                                                           182;
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S53163
e antig
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#formal_name hepatitis B virus, HBV
isolate patient Licheri-3'90
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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e antigen precursor / core antigen -
(isolate patient Licheri-3'90)
HBe antigen precursor / HBc antigen;
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                                                                                                                                                                                                                                                                                           Conservative
08-Sep-1997
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#product core antigen #status predicted #label EAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl terminal propeptide #link EAG #status
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                                                                                                                                                                                                                                                                                           Score 1370; DB 2; 1
Pred. No. 1.36e-201;
1; Mismatches 1;
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hepatitis B virus
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                           ##residues 1-212 ##label LAI
##cross-references EMBL:X65257; NID
##experimental_source subtype ayw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:X85256; NID:g736050; PID:g736052
##experimental_source isolate patient Vittorina/92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESQC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%;
11 Similarity 98.9%;
182; Conservation
                                                                                                                                                                                                                                        e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient C)

HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen

#formal_name hepatitis B virus, HBV subtype ayw, patient C

20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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#superfamily hepatitis B virus core antigen
alternative initiators; core protein
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S53112
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#formal_name hepatitis B virus, HBV
isolate patient Vittorina'92
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                             Sequence analysis
                                                                                                                                            submitted to the EMBL
                                                                                                                                                                         Lai, M.E.; Mazzoleni,
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                                                                                                          ubmitted to the EMBL Data Library, March squence analysis of HBV genomes isolated HBsAg negative chronic liver disease.
                                                                                                                                                             Porru,
                                                                                                                                                                                                                        08-Sep-1997
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to the EMBL Data |
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Pred. No. 2.01e-201;
1; Mismatches 1;
                                            NID:g59429; PID:g59431
                                                                                                                                                                           A.P.;
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##experimental_source isolate patient Chighine-2'86
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              LCWGDLMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFKQLLWFHISCLTFGRETVIEYL 148
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1 Similarity 98.4%;
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Similarity 98.4%;
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#formal_name hepatitis B virus, HBV
isolate patient Chighine-2'86
08-Jul-1995 #sequence_revision 03-A
08-Sep-1997
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e antigen precursor / core antigen -
(isolate pattent Chighine-2'86)
HBe antigen precursor / HBC antigen;
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                                                                                                                                       Score 1369; DB 2; 1
Pred. No. 2.01e-201;
3; Mismatches 0;
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181; Conser
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e antigen precursor / core antigen - hepatitis B virus
(isolate patient Chighine-1'85)
HBe antigen precursor / HBc antigen; pre-C/C antigen
core antigen; e antigen
#formal_name hepatitis B virus, HBV
isolate patient Chighine-1'85
.08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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HBe antigen precursor / HBc antigen; pre-C/C antigen core antigen; e antigen

#formal_name hepatitis B virus, HBV isolate patient Ferracuti-2'90

08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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larity 98.4%;
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alternative initiators; core protein
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                                                                                                                                                                                                      ##residues 1-212 ##label LAI
##cross-references EMBL:X85316; NID:g736208; PID:g736210
##experimental_source isolate patient patient Glordo'84
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S53112
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08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
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e antigen precursor / core antigen -
(isolate patient Giordo 84)
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#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

jth 212 #molecular-weight 24376 #checksum 390
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Data Library, March
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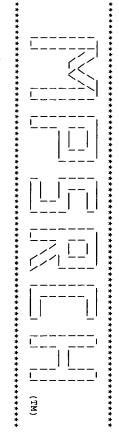
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##residues 1-183 ##label LAI
##residues 1-183 ##label LAI
##cross-references EMBL:x85275; NID:g736057; PID:g736060
##experimental_source isolate patient Muresu'89
##experimental_source isolate patient Muresu'89
##experimental_source isolate patient Muresu'89
##orte due to a stop codon between the alternative initiatiors
##note the e antigen precursor cannot be produced
                                                                                        121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRTPRRRTPSPRRRRSQSPRRRRSQSRE 180
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                                   181 SQC 183
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SQC
 303
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S53112
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Dec 16 13:37:17 1999; MasPar time 10.33 Seconds 829.075 Million cell updates/sec

Title:

Description: Perfect Score: >US3890-1-38183 (1-303) from us3890-1-38183.pep 2263 1 MDIDPYKEFGATVELLSFLP......RRRRSQSPRRRRSQSRESQC 303

Scoring table:

PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 48.698; Variance 104.355; scale 0.467

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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5.02e-02 5.02e-02	2.13e-02	2.13e-02	8.93e-03	8.93e-03	8.93e-03	1.60e-02	1.60e-02	6.67e-03	6.67e-03	2.75e-03	2.75e-03	3.70e-03	2.04e-03	2.04e-03	6.12e-04	4.52e-04	9.70e-05	2.17e-06	8.21e-08	1.38e-12

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Query Match 60.7%; Score 1374; DB 1; Length 183; Best Local Similarity 100.0%; Pred. No. 5.57e-234;	L; V01460; G62278; ALT_INIT. L; X02496; -; NOT_ANNOTATED_CDS.; A03711; NKVLAH. ; A03712; NKVLBH. m; PF00906; Hepatitis_core; 1. E PROTEIN; REPEAT. EART 170 179 EART 170 177 EART 170 177 FLICT 33 33 T -> N (I FLICT 80 80 80 A -> I (I FLICT 183 AA; 21116 MW; 2AE7417	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE: 81012091.  GALIBERT F., MANDART E., FITOUSSI F., TIOLLAIS P., CHARNAY P.;  "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  cloned in E. coll.";  NATURE 281:646-650(1979).  [2]  SEQUENCE FROM N.A. (CLONE PHB320).  MEDLINE: 85204397.  BICHKO V., PUSHKO P., DREILINA D., PUMPEN P., GREN E.;  "Subtype ayw variant of hepatitis B virus. DNA primary structure analysis.";  FEBS LETT. 185:208-212(1985).	RESULT 1  ID CORA_HPBVY STANDARD; PRT; 183 AA.  AC P03146; DT 21-JUL-1986 (REL. 01, CREATED) DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE) DE CORE ANTIGEN. GN C. OS HEPATITIS B VIRUS (SUBTYPE AYW). OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

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TONG S., LI J., VITVITSKI L., TREPO C.;

"Active heparitis B virus replication in the associated with viral variants containing an
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Pred. No. 7.55e-231;
5; Mismatches 4;
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P03147;
21-JUL-1986 (REL. (
21-JUL-1986 (REL. (
01-OCT-1989 (REL.
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01-AUG-1990 (F
01-FEB-1991 (F
CORE ANTIGEN.
SEQUENCE FROM N.A.
MEDLINE; 89010694.
OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO I
MIYAKAWA Y., MAYUMI M.;
"Typing hepatitis B virus by homology in nucleotide
comparison of surface antigen subtypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P17392;
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PASEK M., GOTO T.,
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EAT 170 17;
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177; Conservation 177; Conservation 177
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ANNOTATION
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Pred. No. 4.36e-229;
5; Mismatches 1;
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                                                                                                                                                                                             ONO Y., ONDA H., SASADA R., IGARASHI K., 9
"The complete nucleotide sequences of the
DNA; subtype adr and adw";
NUCLEIC ACIDS RES. 11:1747-1757(1983).
                                                                                                                                                                                                                                                                                                                                                                P03150; P03151;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
MEDLINE; 89010694.
OKAMOTO H., TSUDA F.,
MIYAKAWA Y., MAYUMI M
                                                                                                    FUJIYAMA A., MIYANOHARA MATSUBARA K.; "Cloning and structural
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                                                                                                                                             MEDLINE; 83246570
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                                                                                                                                                                                                                                                                                                   HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADRA), AND HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN INDONESIA/PIDW420). VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
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176; Conser
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183 AA;
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                                                                            11:4601-4610(1983)
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96.2%;
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            SAKUGAWA H.,
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                                                                                                                             A., NOZAKI C., YONEYAMA T., OHTOMO
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Pred. No. 1.52e-226;
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pl7391;
01-AUG-1990 (REL. 1
01-AUG-1990 (REL. 1
01-FEB-1991 (REL. 1
CORE ANTIGEN
HEPATITIS B VIRUS (
VIRUSES; RETROID VI
                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
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OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOEWIGNJO R.I., IMAI MIYAKAWA Y., MAYUMI M.;

"TypAng A Patitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes.";

J. GEN. VIROL. 69:2575-2583(1988).
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EMBL; X01587; G59407; -
EMBL; D00331; -; NOT_ANNOTATED_CDS.
EMBL; D00331; V-LA5.
PIR; A93460; NKVLA5.
PIR; B93460; NKVLA4.
PIR; C28925; NKVLJ3.
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J. GEN. VIROL. 69:2575-2583(1988).
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                   EMBL; D00329; -; NOT_ANNOTATED_CDS
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170
183 AA;
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VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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P03149;
21-JUL-1986 (REL.
21-JUL-1986 (REL.
01-OCT-1989 (REL.
CORE ANTIGEN.
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CORE PROTEIN;
REPEAT 16
REPEAT 17
                                                                                                                                                              PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                          ONO Y., ONDA H., SASADA R., IGARASHI K., 19 "The complete nucleotide sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                   "The complete nucleotide sequences of DNA; subtype adr and adw."; NUCLEIC ACIDS RES. 11:1747-1757(1983).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A MEDLINE; 83168919
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                                                     MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
CWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLV
                                          MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAIL
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176; Conse
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RETROID V
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162 16
170 17
                                                                                                                               185 AA;
                                                                                                                                         164
172
                                                                                   58.4%; ilarity 96.2%; Conservative
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01, LAST SEQUENCE UPDATE)
12, LAST ANNOTATION UPDATE)
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179
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96.2%;
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
                                                                                   Score 1321; DB 1;
Pred. No. 1.31e-223;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1322; DB 1;
Pred. No. 8.34e-224;
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Best Local Similarity 93.5%;
Matches 173; Conservative
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CORA_HPBVT STAN
CO5495;
01-NOV-1995 (REL. 3
01-NOV-1995 (REL. 3
01-NOV-1995 (REL. 3
CORE ANTIGEN.
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P29178;
01-DEC-1992 (REL.
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01-DEC-1992 (REL.
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VIRUSES; R
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BHAT R.A., ULRICH P.P., VYAS G.N.;
"Molecular characterization of a new varia persistently infected homosexual man.";
HEPATOLOGY 11:271-276(1990).
                           "Identification of a new hepatitis that expresses HBV surface antigen J. GEN. VIROL. 74:1627-1632(1993).
                                                                                                                         NAUMANN H., SCHAEFER GERLICH W.H.;
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32, LAST ANNO
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22461 MW; AF3DB5F3 CRC32;
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ANNOTATION UPDAT
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Pred. No. 3.06e-222;
9; Mismatches 3;
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subtype
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adw4.
                                                                       ) genotype from Brazil
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                  01-OCT-1989
01-OCT-1989
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                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               CORA_HPBVL
P12901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                              PFAM;
CORE F
                                                 EMBL;
PIR; /
                                                                                                                                                          "The complete nucleotide sequence virus isolated from a naturally in J. GEN. VIROL. 69:1383-1389(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                         HARRISON T.J.;
                                                                                                                                                                                                   VAUDIN M.,
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                           VIRUSES;
                                                                                                                                                                                                                                                    HEPATITIS B VIRUS (STRAIN
                                                                                                                                                                                                                                                                        CORE ANTIGEN
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                             ;; D00220; D1000603; -.
A28885; NKVLCP.
;; PF00906; Hepatitis_core;
;; PROTEIN; REPEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN;
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191
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212 ;
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                                                                                                                                                                                                                                                                                (REL.
(REL.
  183 AA;
          162
170
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larity 92.9%;
Conservative
                                                                                                                                                     REPEAT
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203
1188
195
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24234
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  20999
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LAST ANNOTATION UPDATE)
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HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
  W.
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Pred. No. 4.79e-22;
10; Mismatches
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3 X 5 AA
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2.
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  1AFF57C9 CRC32;
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P17099;
01-AUG-1990 (REL. 1
01-AUG-1990 (REL. 1
01-AUG-1992 (REL. 2
CORE ANTIGEN.
C.
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P03148;
21-JUL-1986
                                                                                                            CORA_HPBV9
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REPEAT
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VALENUUELA P., QUIROGA M., ZALDIVAR J., GRAY P.,

(IN) FIELD B.N., JAENISCH R., FOX C.F. (EDS.);

ANIMAL VIRUS GENETICS, PP.57-70, ACADEMIC PRESS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORE
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15-DEC-1998
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VIRUSES; RETROID V
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                                                                                                                                                                                         RESQC
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11 Similarity 95.7%;
177; Conservation
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l Similarity 94.5%;
173; Conservative
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185 AA;
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(REL.
                                                                                                                STANDARD;
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23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21304 MW;
                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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HEPADNAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE UP
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Pred. No. 1.76e-220;
4; Mismatches 2;
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Pred. No. 4.55e-221;
6; Mismatches 4;
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Best Local :
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P03152;
21-JUL-1986
21-JUL-1986
15-DEC-1998
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VIRUSES; R
[1]
                                                                                                                                                                                               WOODCHUCK HEPATITIS VIRUS 1 (WHV 1),
WOODCHUCK HEPATITIS VIRUS 7 (WHV 7),
WOODCHUCK HEPATITIS VIRUS 59 (WHV 59), AND
WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE)
VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHO
VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHO
                                                                                                                                                                                                                                                                           CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                    SEQUENCE FROM N.A.
SPECIES-WOODCHUCK HEPATITIS
MEDLINE; 88101359.
COHEN J.I., MILLER R.H., ROS
                                                                                                GALIBERT F., CHEN T.N., MANDART E.;
"Nucleotide sequence of a cloned woodchuck hepatitis virus comparison with the hepatitis B virus sequence.";
J. VIROL. 41:51-65(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S10381; NKVLKS.
PFAM; PF00906; Hepatitis_core;
CORE PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM KOECHEL H.G.,
                                                                                                                                                 SPECIES=WOODCHUCK HEPATITIS MEDLINE; 82216969.
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOBCHEL H.G., SCHUELER A., LOTTMANN S., THOMSSEN R., SUBMITTED (FEB-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
  "Sequence comparison of woodchuck hepatitis shows conservation of the genome.";
                           PURCELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                           ANTIGEN
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177; Conse
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RETROID V
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95.2%;
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HEPADNAVIRIDAE; OR
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Pred. No. 2.75e-220;
                                                             VIRUS
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Best Local Similarity
Matches 126; Conser
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EMBL; M18752; G336140; -.
EMBL; M19183; G336145; -.
EMBL; J04514; G336149; -.
PIR; G33397; NKVLCT.
PIR; C32397; NKVLC4.
PIR; C32397; NKVLC4.
PIR; C32397; NKVLC4.
PIR; C32397; NKVLC4.
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P03153;
21-JUL-1986 (
21-JUL-1986 (
01-JAN-1990 (
CORE ANTIGEN:
                                        "Nucleotide sequence of an infecground squirrel hepatitis virus. J. VIROL. 51:367-375(1984).
                                                                                                        MEDLINE; 84
SEEGER C.,
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GIRONES R., COTE P.J., HORNBUCKLE W.E., TENNANT B.C., PURCELL R.H., MILLER R.H.;
Complete nucleotide sequence of a molecular clone of hepatitis virus that is infectious in the natural host PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
                                                                                                                                                                                                                     GROUND
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SPECIES-WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
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84267998.
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                                                                                                             VARMUS
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HEPADNAVIRIDAE;
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Pred. No. 3.;
25; Mismatch
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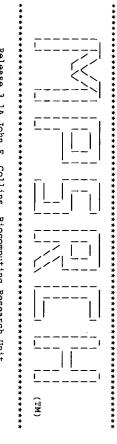
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Query Match 41.2%;
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Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORA_WHV8 P06433;
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"Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
evolutional relationship between hepadnaviruses.";
J. VIROL. 56:978-986(1985).
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                                                                                                        PFAM; PF00906; Hepatitis_core; CORE PROTEIN; REPEAT.
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VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS
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Local Similarity 68.1%;
es 128; Conservative
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204
217 AA;
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Score 933; DB 1; Le Pred. No. 3.00e-148; 26; Mismatches 33;
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Pred. No. 1.92e-148;
22; Mismatches 32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 13:38:08 1999; MasPar time 21.36 Seconds

Run on: Thu Dec 16 13:38:08 1999; MasPar time 21.36 Seconds 774.258 Million cell updates/sec Tabular output not generated.

Title: vUS3890-1-38183
Description: (1-303) from us3890-1-38183.pep
Perfect Score: 2263
Sequence: 1 MDIDPYKEFGATVELLSFLP.......RRRRSQSPRRRRSQSRESQC 303
Scoring table: PAM 150
Gap 11

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.887; Variance 106.690; scale 0.439

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19 20	17 18	16	13 14	11 12	10	, œ	7	თ თ	4	ω	2	_ ب	Result
1363 1363	1364 1363	1366	1369 1368	1369 1369	1370	1370	1372	1374 1373	1374	1373	1373	1375	Score
60.2	60.3	60.4	60.5	60.5	60.5	60.5	60.6	60.7 60.7	60.7	60.7	60.7	60.8	Query
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Q68014 Q68012	Q67989 Q68048	Q68070 Q68030	Q68032 Q68010	Q67872 Q67984	Q68025	Q68066	011884	Q89597 067876	Q68020	Q68008	Q89437	Q89656	ID
PRE-C/CORE. PRE-C/CORE.	X, PREC AND C	PRE-C/CORE. PRE-C/CORE.	PRE-C/CORE. PRE-C/CORE.	PRE C/C ORF. PRE-C/CORE.	PRE-C/CORE.	0	ANTIGEN	HBCAG.	PRE-C/CORE.	X, PREC AND C	X, PREC AND C	PRE-C/CORE.	Description
	GENES (M					GENES (L	PRECURSOR			GENES (F	GENES (C		
5.10e-219 5.10e-219	3.34e-219 5.10e-219	1.43e-219 1.43e-219	3.98e-220 6.09e-220	3.98e-220 3.98e-220	2.60e-220	N	1.11e-220	4.75e-221 7.27e-221	4.75e-221	7.27e-221	7.27e-221	3.10e-221	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	12
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4 Q81115	4 Q68042				4 Q68023			_	4 067912		4 068037	4 067997	4 Q89719	4 067946	4 089531	4 068045	4 068077	4 068075	4 Q68053	4 096845	4 068016	4 089446	4 068051	4 06/980
HBEAG, HBCAG.	PRE-C/CORE.	AND C GENES (	AND C	AND C GENES (	AND C GENES (	PRE-C/CORE.	PRECORE PROTEIN PRECUR	X, PREC AND C GENES (T	PRE-CORE/CORE PROTEIN.	AND C GENES (	PREC AND C	C GENES (	PRE-C/CORE.	C ANTIGEN.	CORE PROTEIN.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	COMPLETE GENOME.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.	PRE-C/CORE.
.87e-2		.87e-	5.87e-215	.84e-	2.51e-215	1.64e-215			4.58e-216		3.00e-216	1.96e-216	8.38e-217	.38e-	5.48e-217		6.54e-218		2.79e-218	1.83e-218		1.83e-218	7.81e-219	5.10e-219

## ALIGNMENTS

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Q89437 PRELIMINARY;
Q89437;
O1-NOV-1996 (TREMBLREL 01, CRI
f 01-NOV-1996 (TREMBLREL 01, LA
T 01-NOV-1998 (TREMBLREL 08, LF
PREC AND C GENES (CASTAA 2
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Best Local
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SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ
EMBL; X895289; G736113; -.
EMBL; X89525; E198055; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 183 AA; 21102 MW; 0C504D47 CR
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
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Pred. No. 7.
1; Mismatc
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Pred. No. 3.10e-221;
1; Mismatches 0;
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01-NOV-1996
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PRE-C/CORE.
HEPATITIS B
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85291; G736119;
PFAM; PF00996; Hepatitis_core; 1.
SEQUENCE 212 AA; 24336 MW; E0E4C243 CRC32;
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VIRUSES; RETROID VIRUSES;
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  VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRTPSPRRRRSQSPRRRRSQSR 299
            VSFGYWIRTDPAYRDPNAPILSTLPETTYVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR 208
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                                                                                                                              Score 1374; DB 14;
Pred. No. 4.75e-221
2; Mismatches 0
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 7.27e-221;
1; Mismatches 0;
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BANKS
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Best Loc
Matches
                                                                                                                                                                                                                                                                                     067876;
067876;
                                                                                                                        PRE C/C ORF.
HEPATITIS B
VIRUSES; RET
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01-NOV-1996
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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SUBMITTED (SEP-1995) TO EMBL/GI
EMBL; X72702; G288930; -.
EMBL; X80925; E198084; -.
PFAM; PF00906; Hepatitis_core;
SEQUENCE 212 AA; 24336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 5
Q89597
Q89597;
SEQUENCE FROM N.A.
STRAIN-PATIENT CI, HBV SUBTYPE AYW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of negative infection."; ARCH. VIROL. 133:385-:
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MEDLINE; 94079539.
PREISLER-ADAMS S., SCHLAYER M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (DEC-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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I similarity 98.9%;
182; Conservative
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                                                                                                                        S B VIRUS.
RETROID VIRUSES;
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                                                                                                                        HEPADNAVIRIDAE;
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Pred. No. 4.
2; Mismatc
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LAST ANNOTATION UPDATE)
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575D20BF
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d. No. 4.75e-221;
Mismatches 0;
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RAO B.S., CASEY J.L., RINAUDO J.
SUBMITTED (MAR-1997) TO EMBL/GEN
EMBL; U95551; G2182120; -.
PFAM: PF00906; Hepatitis_core; 1
SEQUENCE 212 AA; 24360 MW; 7
              Q68066;
01-NOV-1996
01-NOV-1998
X, PREC AND
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PFAM: PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24348 MW; 6ED741BE CRC32;
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01-JUL-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
HEPATITIS B VIRUS
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182; Conser
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(TREMBLREL.
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larity 98.9%;
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EMBL/GENBANK/DDBJ
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                                                                                                                                                                                                                                      Score 1372; DB 14; L
Pred. No. 1.11e-220;
~ wismatches 0;
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LAST SEQUENCE UPDATE)
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Pred. No. 7.27e-221;
2; Mismatches 0;
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STRAIN-PATIENT LICHERI-2'8',
A LAI M.E., MAZZOLENI A.P., PORRU A., BALLONG LAIM.E., MAZZOLENI A.P., PORRU A., BALLONG LAIM. BALLONG LAIM. BELLONG LAIM. BELL
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PRE-C/CORE.
PRE-C/CORE.
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Q68068;
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LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA E
EMBL; X85315; G736207; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;
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ilarity 98.4%;
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98.9%;
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Pred. No. 2.60e-220;
1; Mismatches 1;
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Pred. No. 2.60e-220;
3; Mismatches 0;
PRT;
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PRE C/C ORF.
HEPATITIS B
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01-NOV-1996
01-NOV-1996
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PRE-C/CORE
                                                                                                                                                                                     STRAIN-PATIENT C, HBSAG POSITIV, HBV SUBTYPE AXW;
LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., E
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X65257; G59431; -
EFRAM; PF00906; Hepatitis_core; 1.
                                                                                                                                                                                                                                                   VIRUSES;
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LAH M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85293; G736126; -.
PFAM; PF00906; Hepatitis core; 1.
SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;
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ESQC
                  VSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR
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181; Conser
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larity 98.9%;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                    Score 1369; DB 14;
Pred. No. 3.98e-220;
2; Mismatches 1;
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Pred. No. 2.60e-220;
1; Mismatches 1;
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01-NOV-1996
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LAMI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X85256; G736052; -.
PFAM; PF00906; Hepatitis core; 1.
SEQUENCE 212 AA; 24322 MW; 83D9780B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-PATIENT CHIGHINE-2'86;
LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X85296; G736139; -.
PFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24308 MW; 69D87B53 CRC32;
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VIRUSES; RETROID
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                                    LCWGDLMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFKQLLWFHISCLTFGRETVIEYL 148
ch 60.5%;
l Similarity 98.9%;
182; Conservative
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98.4%;
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                                                                                                                                                                                                                                       Score 1369; DB 14;
Pred. No. 3.98e-220;
3; Mismatches 0;
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Pred. No. 3.98e-220;
1; Mismatches 1;
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83D9780B CRC32;
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Query Match 60.4%;
Best Local Similarity 98.9%;
Matches 182; Conservative
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Best Local
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PRE-C/CORE.
HEPATITIS B
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Q68010;
01-NOV-1996
01-NOV-1996
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SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ
EMBL; X85285; G736100; -.
EFAM; PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24292 MW; 04A4D12D CF
                                                                                          STRAIN-PATIENT GIORDO'84;
LAMI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BEMBL; X85316; G736210; -
PFAM: PF00906; Hepatitis_core: 1.
SEQUENCE 212:AA; 24376 MW; 80F52D0F CRC32;
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Q68070;
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HEPATITIS E
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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1 Similarity 98.4%;
181; Conservati
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8 (TREMBLREL. 08,
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Pred. No. 6.09e-220;
2; Mismatches 1;
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LAST SEQUENCE UI
LAST ANNOTATION
  Score 1366; DB 14;
Pred. No. 1.43e-219;
1; Mismatches 1;
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LAST SEQUENCE UPDATE)
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Indexing Officer: JFUNSTEN - JAMES FUNSTEN

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